

(TM)

Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
1	673	83.1	131	2 S31577	Ig kappa chain - mous	5.35e-87
2	659	81.4	112	2 S20273	Ig kappa chain v regi	1.00e-84
3	653	80.6	142	2 S29022	Ig kappa chain v regi	9.42e-84
4	648	80.0	113	2 S30560	Ig kappa chain v regi	6.09e-83
5	647	79.9	133	2 S23230	Ig kappa chain precu	8.84e-83
6	646	79.8	112	2 A55491	proteolytic antibody	1.28e-82
7	646	79.8	132	2 C32533	Ig kappa chain precu	1.28e-82
8	637	78.6	112	2 S46259	Ig kappa chain v regi	3.68e-81
9	636	78.5	140	2 S26582	Ig kappa chain precu	5.35e-81
10	635	78.4	114	2 S49572	Ig kappa chain precu	7.76e-81
11	634	78.3	126	2 S40312	Ig kappa chain - huma	1.13e-80
12	633	78.1	133	1 K2HURP	Ig kappa chain precu	1.64e-80
13	632	78.0	112	2 B49060	Ig light chain v regi	2.37e-80
14	631	77.9	111	2 S20709	Ig kappa chain v regi	3.44e-80
15	630	77.8	103	2 P11056	Ig light chain v regi	5.00e-80
16	630	77.8	112	2 A26317	Ig kappa chain v regi	5.00e-80
17	628	77.5	112	2 G46317	Ig kappa chain v regi	1.05e-79
18	625	77.2	112	2 F36317	Ig kappa chain v regi	3.22e-79
19	625	77.2	113	1 KVM57S	Ig kappa chain v regi	3.22e-79
20	625	77.2	118	2 S40374	Ig kappa chain - huma	3.22e-79
21	623	76.9	112	2 B26317	Ig kappa chain v regi	6.77e-79
22	621	76.7	112	2 E26317	Ig kappa chain v regi	1.43e-78
23	621	76.7	133	1 A24452	Ig kappa chain precu	1.43e-78

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#cross-references MUID:90111618
#accession F30560
#molecule_type mRNA
#residues 1-112 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-23 #region framework 1\
24-39 #region complementarity-determining 1\
40-54 #region framework 2\
55-61 #region complementarity-determining 2\
62-93 #region framework 3\
94-102 #region complementarity-determining 3\
103-112 #region framework 4\
SUMMARY
#length 112 #checksum 8934
Query Match 81.4%; Score 659; DB 2; Length 112;
Best Local Similarity 81.3%; Pred. No. 1.00e-84;
Matches 91; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Db 1 DVNMTQPLTSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPKRLIYLVSKLD 60
QY 1 DVNMTQSPPLSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 61 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEIK 112
QY 61 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEIK 112

RESULT 3
ENTRY S22902 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S22902
REFERENCE S22902
#authors Chastagner, P.; These, J.; Zouali, M.
#journal Gene (1991) 101:305-306
#title Cloning of a gene encoding a lupus-associated human
autoantibody V(K) region using the polymerase chain
reaction and degenerate primers.
#cross-references MUID:91276289
#accession S22902
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-142 #label CHA
#cross-references EMBL:X56510
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 142 #molecular-weight 15579 #checksum 227

Query Match 80.6%; Score 653; DB 2; Length 142;
Best Local Similarity 84.7%; Pred. No. 9.42e-84;
Matches 94; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Db 32 DVNMTQSPPLSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPKRLIYLVSKNRD 91
QY 1 DVNMTQSPPLSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 92 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEI 142
QY 61 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEI 111

RESULT 4
ENTRY F30560 #type fragment
TITLE Ig kappa chain V region (28.4.10A) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change
20-Mar-1998
ACCESSIONS F30560
REFERENCE A30560

#cross-references MUID:90111062
#accession F30560
#molecule_type preliminary
#residues 1-113 #label MAT
#cross-references GB:M24273; NID:g197081; PID:g197082
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 113 #checksum 1877
Query Match 80.0%; Score 648; DB 2; Length 113;
Best Local Similarity 82.1%; Pred. No. 6.09e-83;
Matches 92; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Db 1 DVNMTQPLTSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPKRLIYLVSKLD 60
QY 1 DVNMTQSPPLSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 61 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEIK 112
QY 61 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEIK 112

RESULT 5
ENTRY S23230 #type fragment
TITLE Ig kappa chain precursor V-J region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
08-Sep-1997
ACCESSIONS S23230
REFERENCE S23230
#authors Kennedy, M.A.
#journal J. Exp. Med. (1991) 173:1033-1036
#title Novel chromosome translocation caused by fusion of
immunoglobulin heavy and light chain V genes in a human B
lymphoblastoid cell line.
#accession S23230
#status preliminary
#molecule_type DNA
#residues 1-133 #label KEN
#cross-references EMBL:X55400; NID:g33999; PID:g34000
GENETICS
#introns 17/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 133 #checksum 2932

Query Match 79.9%; Score 647; DB 2; Length 133;
Best Local Similarity 84.8%; Pred. No. 8.84e-83;
Matches 95; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Db 21 DVNMTQSPPLSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPKRLIYLVSKNRD 80
QY 1 DVNMTQSPPLSLVLTIGQPASISCKSSQSLVYRNGKTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 81 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEIK 132
QY 61 SGVDPRTGSGSGTDFTLKISRVAEDLVGYVYCMQGTHTPFTFGGQTKLEIK 112

RESULT 6
ENTRY A55491 #type complete
TITLE proteolytic antibody light chain - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change
03-May-1996
ACCESSIONS A55491

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[illegible]

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RESULT      9
ENTRY
TITLE      Ig kappa chain precursor V region (O-81vL) - human (fragment)
ORGANISM   Homo sapiens
DATE       29-Jan-1998
#revision  06-Feb-1998
#text_change

ACCESSIONS S22658
REFERENCE   S22657
AUTHORS    Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
JOURNAL    Nucleic Acids Res. (1992) 20:2601
#journal   Variable regions of a human anti-DNA antibody O-81 possessing
#title     lupus nephritis-associated idiotype.

#accession S22658
#molecule_type mRNA
#residues  1-140
#label     HIR
#cross-references EMBL:X59135
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin

FEATURE
1-19         #domain signal sequence
20-140       #product Ig kappa chain (fragment)
#label       MAR
#status      predicted
#length     140
#checksum    5056

SUMMARY

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[illegible]

RESULT	10
ENTRY	S49572
TITLE	Ig kappa chain precursor - human (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 20-Mar-1998
ACCESSIONS	S49572
REFERENCE	S49571
#authors	Giachino, C.; Padovan, E.; Lanzavecchia, A.
#submission	submitted to the EMBL Data Library, November 1994

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#description k+l+ dual receptor B cells are present in the human
#accession S49572
##status preliminary
##molecule_type mRNA
##molecule 1-114 #label GIA
##residues 1-114 #label GIA
##cross-references EMBL:246626; NID:g575261; PID:g575262
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 114 #checksum 9334

Query Match 78.4%; Score 635; DB 2; Length 114;
Best Local Similarity 82.3%; Pred. No. 7,76e-81;
Matches 93; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

Db 1 DVWMTQSPVLTIGQPASISCRSSQSLVSDGNTYLNWFOQRPGQSPRLIYKVSNRD 60
QY 1 DVWMTQSPVLTIGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60
Db 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYVCMQFTHYP-YTFGGGKLEIK 113
QY 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYVCMQFTHYP-YTFGGGKLEIK 112

RESULT 11
ENTRY S40312 #type complete
TITLE Ig kappa chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
08-Sep-1997
ACCESSIONS S40312
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. (1993) 23:3248-3271
Expressed human immunoglobulin chi genes and their
hypermutation.
#accession S40312
#status preliminary; translation not shown
#residues 1-126 #label KLE
#molecule_type mRNA
#cross-references EMBL:X72422; NID:g441312; PID:g441313
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 126 #molecular-weight 13744 #checksum 4861

Query Match 78.3%; Score 634; DB 2; Length 126;
Best Local Similarity 80.4%; Pred. No. 1.13e-80;
Matches 90; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 14 DVMTQTPVLTIGQPASISCRSSQSLVSDGNTYLNWFOQRPGQSPRLIYKISNR 73
QY 1 DVWMTQSPVLTIGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60
Db 74 SGVDPFRFSGSGGDTFTLKISVEAEDGVYVCMQATQFPYTFGGGKLEIK 125
QY 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYVCMQFTHYPYTFGGGKLEIK 112

RESULT 12
ENTRY K2HURP #type complete
TITLE Ig kappa chain precursor V-II region (RPMI) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
15-Aug-1997
ACCESSIONS A01890
REFERENCE A9388
#authors Klobbeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.;
Zachau, H.G.
#journal Nucleic Acids Res. (1985) 13:6499-6513
#title Human immunoglobulin kappa light chain genes of subgroups II
and III.
#cross-references MUID:86041852
#accession A01890
#molecule_type DNA

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##residues 1-133 #label KLO
##note the sequence was determined from the differentiated gene
GENETICS
#gene GDB:IGKV2
#map_position 2p12-2p12
#introns 17/1
COMPLEX An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily immunoglobulin V region; immunoglobulin homology
heterotetramer; immunoglobulin
CLASSIFICATION
KEYWORDS #domain signal sequence #status predicted #label SIG\
FEATURE #product Ig kappa chain V-II region (RPMI) #status
1-20 predicted #label MAT\
21-133 #region framework 1\
36-115 #domain immunoglobulin homology #label IMM\
44-59 #region complementarity-determining 1\
60-74 #region framework 2\
75-81 #region complementarity-determining 2\
82-113 #region framework 3\
114-122 #region complementarity-determining 3\
123-133 #region framework 4\
43-113 #disulfide-bonds #status predicted
SUMMARY #length 133 #molecular-weight 14707 #checksum 4055

Query Match 78.1%; Score 633; DB 1; Length 133;
Best Local Similarity 83.0%; Pred. No. 1.64e-80;
Matches 93; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Db 21 DVWMTQSPVLTIGQPASISCRSSQSLVSDGNTYLNWFOQRPGQSPRLIYKVSNRD 80
QY 1 DVWMTQSPVLTIGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60
Db 81 SGVDPFRFSGSGGDTFTLKISVEAEDGVYVCMQTHWTFGGGKVEIK 132
QY 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYVCMQFTHYPYTFGGGKLEIK 112

RESULT 13
ENTRY B49060 #type fragment
TITLE Ig light chain V region, phenyl phosphonate hapten-specific
catalytic monoclonal antibody (isobzyme) 20G9 - mouse
(fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
16-Aug-1996
ACCESSIONS B49060
REFERENCE A49060
#authors Angeles, T.S.; Smith, R.G.; Darsley, M.J.; Sugawara, R.;
Sanchez, R.I.; Kanten, J.; Schultz, P.G.; Martin, M.T.
#journal Biochemistry (1993) 32:12128-12135
#title Isozymes: structurally and mechanistically similar
catalytic antibodies from the same immunization.
#cross-references MUID:94032348
#accession B49060
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-112 #label ANG
#experimental_source hybridoma cell
#note sequence extracted from NCBI backbone (NCBIP:140373)
#superfamily immunoglobulin V region; immunoglobulin homology
CLASSIFICATION
KEYWORDS immunoglobulin
SUMMARY #length 112 #checksum 1098

Query Match 78.0%; Score 632; DB 2; Length 112;
Best Local Similarity 75.9%; Pred. No. 2.37e-80;
Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

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Db 1 EIVLTQSPPSVIVTGPESVTSICRSSLHSGNTYLYWFLQRPQSPQVLIYRMSNLA 60
 QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLYWFLQRPQSPQVLIYVSKLE 60
 Db 61 SGVPDRFSGSGTFTLRISRVDAEDGVVYICQYLEIPYTFGGGKLEIK 112
 QY 61 SGVPDRFSGSGTFTLRISRVDAEDGVVYICQYLEIPYTFGGGKLEIK 112

RESULT 14
 ENTRY TITLE
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCE
 #authors
 #submission
 #description
 #accession
 #status
 #molecule_type
 #residues
 #cross-references
 CLASSIFICATION
 KEYWORDS
 SUMMARY

S20709 #type complete
 Ig kappa chain V region - mouse
 #formal_name Mus musculus #common_name house mouse
 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
 08-Sep-1997
 S20709
 S20706
 Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.;
 Harris, W.J.; Carr, F.J.; Osborn, N.J.; Glennie, M.J.;
 Richards, N.G.; Robinson, J.A.
 Submitted to the EMBL Data Library, April 1992
 Binding specificity and variable region sequences of two
 monoclonal antibodies that recognise a beta-turn forming
 peptide containing alpha-methylproline.
 S20709 preliminary
 #molecule_type DNA
 #residues 1-111 #label BRE
 #cross-references EMBL:211917; NID:G52655; PID:G52656
 #superfamily immunoglobulin V region; immunoglobulin homology
 heterotetramer; immunoglobulin
 #length 111 #molecular_weight 12122 #checksum 3705

Query Match 77.9%; Score 631; DB 2; Length 111;
 Best Local Similarity 81.1%; Pred. No. 3.44e-80;
 Matches 90; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Db 1 DIQLTQSPPLSVITIGQPASISCRSSQSLHSGNTYLYWFLQRPQSPKRLIYVSKLD 60
 QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLYWFLQRPQSPQVLIYVSKLE 60
 Db 61 SGVPDRFSGSGTFTLRISRVDAEDGVVYICQYLEIPYTFGGGKLEIK 111
 QY 61 SGVPDRFSGSGTFTLRISRVDAEDGVVYICQYLEIPYTFGGGKLEIK 111

RESULT 15
 ENTRY TITLE
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCE
 #authors
 #journal
 #title
 #accession
 #status
 #molecule_type
 #residues
 #experimental_source
 CLASSIFICATION
 KEYWORDS
 SUMMARY

PHI056 #type fragment
 Ig light chain V region (clone 111-c2) - mouse (fragment)
 #formal_name Mus musculus #common_name house mouse
 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
 15-Jun-1996
 PHI056
 PH0971
 Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. (1992) 176:761-779
 Both IgM and IgG anti-DNA antibodies are the products of
 clonally selective B cell stimulation in (NZB x NZW)F1
 mice.
 PHI056
 #molecule_type mRNA
 #residues 1-103 #label TIL
 #experimental_source B cell, strain [NZB x NZW]F1
 #superfamily immunoglobulin V region; immunoglobulin homology
 immunoglobulin
 #length 103 #checksum 3621

Query Match 77.8%; Score 630; DB 2; Length 103;
 Best Local Similarity 83.5%; Pred. No. 5.00e-80;
 Matches 86; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Db 1 DVVMTQSPPLSVITIGQPASISCRSSQSLHSGNTYLYWFLQRPQSPKRLIYVSKLE 60

QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLYWFLQRPQSPQVLIYVSKLE 60
 Db 61 SGVPDRFSGSGTFTLRISRVDAEDGVVYICQYLEIPYTFGGGKLEIK 103
 QY 61 SGVPDRFSGSGTFTLRISRVDAEDGVVYICQYLEIPYTFGGGKLEIK 103

Search completed: Thu Jan 14 17:12:05 1999
 Job time : 13 secs.

Result No.	Query Match	Score	Length	DB	ID	Description	Pred. No.	
1	78.1	633	133	1	KV2F_HUMAN	IG KAPPA CHAIN V-II RE	1.99e-12	
2	77.2	625	113	1	KV2F_MOUSE	IG KAPPA CHAIN V-II RE	1.69e-11	
3	75.7	613	113	1	KV2B_HUMAN	IG KAPPA CHAIN V-II RE	1.32e-11	
4	74.3	602	113	1	KV2D_HUMAN	IG KAPPA CHAIN V-II RE	5.82e-11	
5	73.5	595	117	1	KV2E_HUMAN	IG KAPPA CHAIN PRECURS	2.80e-11	
6	72.8	590	115	1	KV2A_HUMAN	IG KAPPA CHAIN V-II RE	4.44e-11	
7	70.5	571	112	1	KV2C_HUMAN	IG KAPPA CHAIN V-II RE	1.60e-10	
8	70.1	568	113	1	KV2G_MOUSE	IG KAPPA CHAIN V-II RE	8.36e-10	
9	68.9	558	112	1	KV2D_MOUSE	IG KAPPA CHAIN V-II RE	2.06e-10	
10	68.1	552	112	1	KV2E_MOUSE	IG KAPPA CHAIN V-II RE	5.60e-10	
11	66.8	541	114	1	KV4A_HUMAN	IG KAPPA CHAIN V-IV RE	2.37e-99	
12	65.9	534	134	1	KV4C_HUMAN	IG KAPPA CHAIN PRECURS	1.10e-97	
13	63.5	514	112	1	KV2A_MOUSE	IG KAPPA CHAIN V-II RE	6.32e-93	
14	63.2	512	113	1	KV2C_MOUSE	IG KAPPA CHAIN V-II RE	1.89e-92	
15	63.0	510	111	1	KV3J_MOUSE	IG KAPPA CHAIN V-III R	5.63e-92	
16	63.0	510	133	1	KV4B_HUMAN	IG KAPPA CHAIN PRECURS	5.63e-92	
17	62.7	508	111	1	KV3H_MOUSE	IG KAPPA CHAIN V-III R	1.68e-91	
18	62.6	507	111	1	KV3L_MOUSE	IG KAPPA CHAIN V-III R	2.90e-91	
19	62.5	506	111	1	KV3M_MOUSE	IG KAPPA CHAIN V-III R	5.01e-91	
20	62.2	504	111	1	KV3U_MOUSE	IG KAPPA CHAIN V-III R	1.49e-90	
21	61.9	501	111	1	KV3S_MOUSE	IG KAPPA CHAIN V-III R	7.68e-90	
22	61.7	500	111	1	KV3R_MOUSE	IG KAPPA CHAIN V-III R	1.33e-89	
23	61.6	499	111	1	KV3O_MOUSE	IG KAPPA CHAIN V-III R	2.29e-89	

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FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 64 74 FRAMEWORK 2.
FT DOMAIN 70 74 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 75 81 FRAMEWORK 3.
FT DOMAIN 82 113 FRAMEWORK 4.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 2DC342B5 CRC32;

Query Match 78.1%; Score 633; DB 1; Length 133;
Best Local Similarity 83.0%; Pred. No. 1.99e-121;
Matches 93; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Db 21 DVVMTQSPPLSYLTGQPASISCRSSQSLVYSDGNVYLNWFGQSPGSPRLIYKYSNRD 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 DVVMTQSPPLSYLTGQPASISCRSSQSLHSGNVLNWLQRGSPGSPQLIYLVSKLE 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 SGVPDRFSGSGSGTDFTLISRVEADGVYVYCMQGTHTMSWTSGQGTKEIK 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 SGVPDRFSGSGSGTDFTLKISGVEADGVYVYCMQGTHTPYPTFGSGTKLEIK 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
ID KV2F_MOUSE STANDARD; PRT; 113 AA.

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Query Match      75.7%; Score 613; DB 1; Length 113;
Best Local Similarity 77.9%; Pred. No. 1.32e-116;
Matches      85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Db      1 DVMVTOSPLFLPTLCEPASICRQSQSLVYRBGYLWYKQPCQSPQLLYLVSKLE 60
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      1 DVMVTOSPPSLVLTGQPASICRQSQSLHSGSNTYLNWLLQRPQSPQLLYLVSKLE 60
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      61 SGVPDRFSGSGGTDFTLKTRVQAEADVGVYCMQATZSPYTFGQGTKLZIK 112
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61 SGVPDRFSGSGGTDFTLKISGVEADVGVYCMQTHPYTFGQGTKEIK 112
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      4
ID      KV2D.HUMAN      STANDARD;      PRT;      113 AA.
AC      P01617;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE      IG KAPPA CHAIN V-II REGION (TEW).
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; PRIMATES.
[1]
RN      SEQUENCE (BENCE-JONES PROTEIN TEW).
RP      MEDLINE; 74149480.
RX      PUTNAM F.W., WHITLEY E.J. JR., PAUL C., DAVIDSON J.N.;
RL      BIOCHEMISTRY 12:3763-3780(1973).
[2]
RN      SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RP      MEDLINE; 73166638.
RX      TERRY W.D., PAGE D.L., KIMURA S., ISOBE T., OSSERMAN E.F.,
RA      GLENNER G.G.;
RL      J. CLIN. INVEST. 52:1276-1281(1973).
CC      -!- THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE
CC      JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC      -!- THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH
CC      PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC      -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
DR      PIR; A01888; K2HUTW.
DR      HSP; P01679; 1CBV.
KW      IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; AMYLOID.
FT      DOMAIN 1 23
FT      DOMAIN 24 39
FT      DOMAIN 40 54
FT      DOMAIN 55 61
FT      DOMAIN 62 93
FT      DOMAIN 94 102
FT      DOMAIN 103 112
FT      DISULFID 23 93
FT      NON_TER 113 113
SQ      SEQUENCE 113 AA; 12316 MW; FC2B2819 CRC32;

Query Match      74.3%; Score 602; DB 1; Length 113;
Best Local Similarity 77.7%; Pred. No. 5.82e-114;
Matches      87; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Db      1 DVMVTOSPLFLPTLCEPASICRQSQSLHSGDGYLNWYKQPCQSPQLLYLVSKLE 60
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      1 DVMVTOSPPSLVLTGQPASICRQSQSLHSGSNTYLNWLLQRPQSPQLLYLVSKLE 60
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      61 SGVPDRFSGSGGTDFTLKISVBEADVGVYCMZALQAPITFGQGTREIK 112
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61 SGVPDRFSGSGGTDFTLKISGVEADVGVYCMQTHPYTFGQGTKEIK 112
      |:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      5
ID      KV2E.HUMAN      STANDARD;      PRT;      117 AA.
AC      P06309;
DT      01-JAN-1988 (REL. 06, CREATED)
DT      01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT      01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE      IG KAPPA CHAIN PRECURSOR V-II REGION (GM507) (FRAGMENT).

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OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 84191506.
 RX KLOBECK H.G., SOLOMON A., ZACHAU H.G.;
 RL NATURE 309:73-76(1984).
 DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
 DR PIR; A01889; K2HUGM.
 DR HSP; P01679; ICBV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION (GM607).
 FT DOMAIN 5 27 FRAMEWORK 1.
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 44 58 FRAMEWORK 2.
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 66 97 FRAMEWORK 3.
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 107 116 FRAMEWORK 4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; E09E9ACC CRC32;

Query Match 73.5%; Score 595; DB 1; Length 117;
 Best Local Similarity 78.6%; Pred. No. 2.80e-112;
 Matches 88; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
 Db 5 DIVVTQSPSLPVTGPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKNRA 64
 QY 1 DIVVTQSPSLPVTGPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 60
 Db 65 SGVPDRFSGSGGTDFTLKISRVAEDGVGYVYCMQGLQTPTFGGQTKVEIK 116
 QY 61 SGVPDRFSGSGGTDFTLKISRVAEDGVGYVYCMQFTHYPTFGGQTKLEIK 112

RESULT 6
 ID KV2A_HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (CUM).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 68242259.
 RA HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 348:1718-1722(1967).
 RN [2]
 RP REVISIONS TO 50; 52; 96 AND 97.
 RX MEDLINE; 70063440.
 RA HILSCHMANN N.;
 RL NATURWISSENSCHAFTEN 56:195-205(1969).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01885; K2HUGM.
 DR HSP; P01607; IIGI.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DISULFID 24 95 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 5500220A CRC32;

Query Match 72.8%; Score 590; DB 1; Length 115;
 Best Local Similarity 77.9%; Pred. No. 4.44e-111;
 Matches 88; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
 Db 2 DIVVTQSPSLPVTGPASISCRSSQSLDSDGNTYLNWLLQKAGOSPOLLITLSYR 61

QY 1 DIVVTQSPSLPVTGPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKL 59
 Db 62 ASGVDPDRFSGSGGTDFTLKISRVAEDGVGYVYCMQRLIEPTFGGQTKLEIR 114
 QY 60 ESGVDPDRFSGSGGTDFTLKISRVAEDGVGYVYCMQFTHYPTFGGQTKLEIK 112

RESULT 7
 ID KV2C_HUMAN STANDARD; PRT; 112 AA.
 AC P01616;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (MIL).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RA DREYER W.J., GRAY W.R., HOOD L.E.;
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 32:353-367(1967).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01887; K2HOML.
 DR HSP; P01679; ICBV.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12055 MW; C487DFDF CRC32;

Query Match 70.5%; Score 571; DB 1; Length 112;
 Best Local Similarity 67.9%; Pred. No. 1.60e-106;
 Matches 76; Conservative 21; Mismatches 14; Indels 1; Gaps 1;
 Db 1 DIVVTQSPSLPVTGPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKNRA 59
 QY 1 DIVVTQSPSLPVTGPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 60
 Db 60 SGVDPDRFSGSGGTDFTLKISRVAEDGVGYVYCMQALQTPITFGGQTKVEIK 111
 QY 61 SGVDPDRFSGSGGTDFTLKISRVAEDGVGYVYCMQFTHYPTFGGQTKLEIK 112

RESULT 8
 ID KV2G_MOUSE STANDARD; PRT; 113 AA.
 AC P01631;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (26-10).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 83178921.
 RA NOVOTNY J., MARGOLIES M.N.;
 RL BIOCHEMISTRY 22:1153-1158(1983).
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT
 CC BINDS DIGOXIN.
 DR PIR; A01914; KVM526.
 DR HSP; P01607; IIGI.
 KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.


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FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; 58372CBE CRC32;

Query Match
Best Local Similarity 70.1%; Score 568; DB 1; Length 113;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Db 1 DVMTQTPLSPVSLGDAQISCRSSQLVHSGNTYLNWYLOKAGQSPKLLIYKVSNR 60
QY 1 DVMTQSPSLVLTGQPASISCRSSQLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCAHLELPYTFGGGKLEIK 112
QY 61 SGVDPFRSGSGGDTFTLKISGVEAEDGVVYCMQFTHYPTFGGKLEIK 112

RESULT 9
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (REL. 02, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (17S29.1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RC TISSUE-HYBRIDOMA;
RX MEDLINE; 85128968.
RA AEBERSOLD R., HERBST H., GRUTTER T., CHANG J.Y., BRAUN D.G.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 365:1375-1383(1984).
CC -I- ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR: A01912; KVM517.
DR HSP: P01679; ICBV.
KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 6A4552AE CRC32;

Query Match
Best Local Similarity 68.9%; Score 558; DB 1; Length 113;
Matches 82; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Db 1 DVMTQAVFNPVLTGTSASISCRSSKSLHSGNTYLYWYLOKQSPQLLIYQMSNLA 60
QY 1 DVMTQSPSLVLTGQPASISCRSSQLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCAHLELPYTFGGGKLEIK 112
QY 61 SGVDPFRSGSGGDTFTLKISGVEAEDGVVYCMQFTHYPTFGGKLEIK 112

RESULT 10
ID KV2D_MOUSE STANDARD; PRT; 112 AA.
AC P01629;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-II REGION (2S1.3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN SEQUENCE.
RX MEDLINE; 83055101.
RA HERBST H., CHANG J.Y., AEBERSOLD R., BRAUN D.G.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 363:1069-1076(1982).
CC -I- THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY
    AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01911; KVM5S1.
DR HSP: P01607; 4FAB.
KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; C16DB265 CRC32;

Query Match
Best Local Similarity 72.3%; Score 552; DB 1; Length 112;
Matches 81; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Db 1 DVMTQAFNPVLTGTSASISCRSSKSLQSKGTYLYWYLOKQSPQLLIYQMSNLA 60
QY 1 DVMTQSPSLVLTGQPASISCRSSQLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCAHLELPYTFGGGKLEIK 112
QY 61 SGVDPFRSGSGGDTFTLKISGVEAEDGVVYCMQFTHYPTFGGKLEIK 112

RESULT 11
ID KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-IV REGION (LEN).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN SEQUENCE.
RX MEDLINE; 76004342.
RA SCHNEIDER M., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:507-557(1975).
RN REVISION TO 9.
RP REVISION TO 9.
RA SALOMON A.;
RL SUBMITTED (AUG-1996) TO THE SWISS-PROT DATA BANK.
CC -I- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01903; K4HULN.
DR HSP: P01607; 1MCP.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 41 55 FRAMEWORK 2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 63 94 FRAMEWORK 3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 113 FRAMEWORK 4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; EEICE0BE CRC32;

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Query Match 66.8%; Score 541; DB 1; Length 114;
 Best Local Similarity 67.3%; Pred. No. 2,37e-99;
 Matches 76; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

Db 1 DIVMTQSPDLSAVLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLIYWASTR 60
 QY 1 DIVMTQSPDLSAVLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLIYWASTR 59

Db 61 EGVDPFRSGSGGDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 113
 QY 60 EGVDPFRSGSGGDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112

RESULT 12
 ID KV4C_HUMAN STANDARD; PRT; 134 AA.
 AC P06314;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-IV REGION (B17).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86041854.
 RA MARSH P., MILLS F., GOULD H.;
 RL NUCLEIC ACIDS RES. 13:6531-6544 (1985).
 RN [2]
 RP REVISION TO 76.
 RA MARSH P.;
 RL SUBMITTED (OCT-1986) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; X02990; G37910;
 DR PIR; A01905; K4HU17.
 DR HSSP; P01607; 21MN.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-III REGION (B17).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 133 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; BB63E06A CRC32;

Query Match 65.9%; Score 534; DB 1; Length 134;
 Best Local Similarity 67.3%; Pred. No. 1.10e-97;
 Matches 76; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

Db 21 DIVMTQSPDLSAVLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLIYWASTR 80
 QY 1 DIVMTQSPDLSAVLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLIYWASTR 59

Db 81 EGVDPFRSGSGGDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 133
 QY 60 EGVDPFRSGSGGDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112

RESULT 13
 ID KV2A_MOUSE STANDARD; PRT; 112 AA.
 AC P01626;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (MOPC 167).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE.
 RX MEDLINE; 79000273.
 RA RUDIKOFF S., POTTER M.;
 RL BIOCHEMISTRY 17:2703-2707 (1978).
 CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS
 CC PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
 CC CHAIN HAS ALSO BEEN DETERMINED.
 DR PIR; A01908; KVM516.
 DR HSSP; P01679; 1CBV.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12349 MW; 84A526D0 CRC32;

Query Match 63.5%; Score 514; DB 1; Length 112;
 Best Local Similarity 68.8%; Pred. No. 6.32e-93;
 Matches 77; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

Db 1 DIVITQDELSPVTSGESVISCSSKSLYKDGKTYLNNWFLQRPQSPQLLIYLMSTRA 60
 QY 1 DIVITQDELSPVTSGESVISCSSKSLYKDGKTYLNNWFLQRPQSPQLLIYLMSTRA 60

Db 61 SGVSDRFGSGSGRTDFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112
 QY 61 SGVSDRFGSGSGRTDFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112

RESULT 14
 ID KV2C_MOUSE STANDARD; PRT; 113 AA.
 AC P01628;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (MOPC 511).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 81052016.
 RA APPELLA E.;
 RL MOL. IMMUNOL. 17:711-718 (1980).
 CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS
 CC PHOSPHORYLCHOLINE.
 DR PIR; A01910; KVM551.
 DR HSSP; P01679; 1CBV.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12496 MW; 7926A2F7 CRC32;

Query Match 63.2%; Score 512; DB 1; Length 113;
 Best Local Similarity 67.9%; Pred. No. 1.89e-92;
 Matches 76; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

Db 1 DIVITQDELSPVTSGESVISCSSKSLYKDGKTYLNNWFLQRPQSPQLLIYLMSTRA 60
 QY 1 DIVITQDELSPVTSGESVISCSSKSLYKDGKTYLNNWFLQRPQSPQLLIYLMSTRA 60

Search completed: Thu Jan 14 17:10:43 1999.
Job time : 9 secs.

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-PBL;

RA ITOH K., SUZUKI T.;

RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; AB006843; D103042; -

DR PFAM; PF00047; 19.

FT NON_TER 118

SQ SEQUENCE 118 AA; 12804 MW; CECE507A CRC32;

Query Match 76.7%; Score 621; DB 4; Length 118;

Best Local Similarity 79.5%; Pred. No. 1.80e-118;

Matches 89; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Db 3 ELVLTQSLPSLVTPGEPASISCRSSQSLHSHNGNFMNDWYLRQRPQSPQLLYIGSNRA 62

QY 1 DVVMTQSPSPSLVTLGQPASISCRSSQSLHSHSGNTYLNWLLQRPQSPQLLYLVSKLE 60

Db 63 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCMQGLQTPYTFGGTGKLEIK 114

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCMQFTHYPYTFGGTGKLEIK 112

RESULT 3

ID P97512 PRELIMINARY; PRT; 249 AA.

AC P97512;

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DE SINGLE CHAIN FV ANTIBODY (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

[1]

RP SEQUENCE FROM N.A.

RA ARTSAENKO O., WEILER E.W., MUENTZ K., CONRAD U.;

RL J. PLANT PHYSIOL. 144:427-429(1994).

RN [2]

RP SEQUENCE FROM N.A.

EX MEDLINE; 96086099.

RA ARTSAENKO O., PEISKER M., ZUR NIEDEN U., FIEDLER U., WEILER E.W.,

RA MUENTZ K., CONRAD U.;

RL PLANT J. 8:745-750(1995).

DR EMBL; Z29480; E283450; -

DR PFAM; PF00047; 19.

FT NON_TER 1

SQ SEQUENCE 249 AA; 26839 MW; 428B904E CRC32;

Query Match 71.2%; Score 577; DB 11; Length 249;

Best Local Similarity 71.4%; Pred. No. 6.59e-108;

Matches 80; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

Db 135 DIETQSPSPVVVPGESVSVISCRSKSLLYSDGSYLFWFQRPQSPQLLYRMSNLA 194

QY 1 DVVMTQSPSPSLVTLGQPASISCRSSQSLHSHSGNTYLNWLLQRPQSPQLLYLVSKLE 60

Db 195 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCMQHREYPLTFGGTGKLEIK 246

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCMQFTHYPYTFGGTGKLEIK 112

RESULT 4

ID O55115 PRELIMINARY; PRT; 119 AA.

AC O55115;

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DE IG KAPPA CHAIN PRECURSOR (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

[1]

RP SEQUENCE FROM N.A.

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-LIVER;

RX MEDLINE; 87110625.

RA CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;

RL J. IMMUNOL. 138:932-939(1987).

DR EMBL; D00080; D1000493; -

KW SIGNAL.

FT SIGNAL.

FT CHAIN 1

FT CHAIN 20

FT NON_TER 119

SQ SEQUENCE 119 AA; 13079 MW; 6B5A6578 CRC32;

Query Match 63.7%; Score 516; DB 11; Length 119;

Best Local Similarity 77.0%; Pred. No. 2.32e-93;

Matches 77; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Db 20 DVVMTQTPSLPSLVTPGEPASISCRSSQSLVHSHNGNTYLNWLLQRPQSPQLLYKVSNRF 79

QY 1 DVVMTQSPSPSLVTLGQPASISCRSSQSLHSHSGNTYLNWLLQRPQSPQLLYLVSKLE 60

Db 80 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCSQSTHYP 119

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCMQFTHYP 100

RESULT 5

ID Q15535 PRELIMINARY; PRT; 100 AA.

AC Q15535;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)

DE V KAPPA (FRAGMENT).

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

[1]

RP SEQUENCE FROM N.A.

RA KATO S., TACHIBANA K., TAKAYAMA N., KATAOKA H., YOSHIDA M.C.,

RA TAKANO T.;

RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; D90161; G1262585; -

DR PFAM; PF00047; 19.

FT NON_TER 1

SQ SEQUENCE 100 AA; 10871 MW; 06A1440D CRC32;

Query Match 63.2%; Score 512; DB 4; Length 100;

Best Local Similarity 79.0%; Pred. No. 2.07e-92;

Matches 79; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Db 1 DVVMTQTPSLPSLVTPGEPASISCRSSQSLHSHSGNTYLNWLLQRPQSPQLLYEVSRRF 60

QY 1 DVVMTQSPSPSLVTLGQPASISCRSSQSLHSHSGNTYLNWLLQRPQSPQLLYLVSKLE 60

Db 61 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCMQIHLP 100

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDGCVVYCMQFTHYP 100

RESULT 6

ID O55116 PRELIMINARY; PRT; 119 AA.

AC O55116;

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DE IG KAPPA CHAIN (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

[1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-LIVER;
RX MEDLINE; 87110625.
RA CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;
RL J. IMMUNOL. 138:932-939(1987).
DR EMBL; D00081; D1000494;
FT NON_TER 119
SQ SEQUENCE 119 AA; 13117 MW; C201F8D8 CRC32;

Query Match 62.3%; Score 505; DB 11; Length 119;
Best Local Similarity 75.0%; Pred. No. 9.46e-91;
Matches 75; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Db 20 DVLMQTPLSPVSLGQASISCRSSOSIVHSNGNTLVLYLKPGOSPQLLIYKVSNR 79
QY 1 DVMTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKLE 60
DB 80 SGVPDFRFGSGGTDFTLKISGVEAEDGVYYCMQFTHYP 119
QY 61 SGVPDFRFGSGGTDFTLKISGVEAEDGVYYCMQFTHYP 100

RESULT 7 PRELIMINARY; PRT; 119 AA.

ID Q55117 AC Q55117
DT 01-JUN-1998 (TREMBREL. 06, CREATED)
DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C; TISSUE-LIVER;
RX MEDLINE; 87110625.
RA CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;
RL J. IMMUNOL. 138:932-939(1987).
DR EMBL; D00082; D1000495;
FT NON_TER 119
SQ SEQUENCE 119 AA; 13117 MW; 7D3761A1 CRC32;

Query Match 62.0%; Score 502; DB 11; Length 119;
Best Local Similarity 76.0%; Pred. No. 4.86e-90;
Matches 76; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Db 20 DAVMTQPLSPVSLGQASISCRSSOSLNSGNTYNWLLQRPGSQPQLIYKVSNR 79
QY 1 DVMTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKLE 60
DB 80 SGVLDPRFGSGGTDFTLKISGVEAEDGVYFCIQVTHVP 119
QY 61 SGVPDFRFGSGGTDFTLKISGVEAEDGVYYCMQFTHYP 100

RESULT 8 PRELIMINARY; PRT; 133 AA.

ID Q61551 AC Q61551
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DE CC49 FAB PRECURSOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA ABERGEL C., PADLAN E.A., KASHMIRI S.V.S., MILENIC D., CALVO B.,
SCHLOW J.;
RL SUBMITTED (JUN-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; M95574; G193215;
DR PFAM; PF00047; 19.
KW SIGNAL.
FT SIGNAL.
FT NON_TER 1 20 POTENTIAL.

FT CHAIN 21 >133 CC49 FAB.
SQ SEQUENCE 133 AA; 14528 MW; F1EA6B5F CRC32;
Query Match 61.9%; Score 501; DB 11; Length 133;
Best Local Similarity 61.9%; Pred. No. 8.39e-90;
Matches 70; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Db 21 DIVMQSPSSLPSVGKEKVTLSCKSSQSLYSNOKNYLAQYQQKPGQPKLIYWASAR 80
QY 1 DVMTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKL 59
DB 81 ESGVDPFRFGSGGTDFTLISVKTEDLVAYVCQYQSYPIFTFGAGTKLVK 133
QY 60 ESGVDPFRFGSGGTDFTLKISGVEAEDGVYYCMQFTHYPFTGGTGLEIK 112

RESULT 9 PRELIMINARY; PRT; 115 AA.

ID Q99826 AC Q99826
DT 01-MAY-1997 (TREMBREL. 03, CREATED)
DT 01-MAY-1997 (TREMBREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE ANTI-HIV-1 GP120 V3 LOOP ANTIBODY DOI42-10 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA DITZEL H.J., PARREN P.W.H.I., BINLEY J.M., SODROSKI J., MOORE J.P.,
BARBAS C.F., BURTON D.R.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U82962; G1800287;
DR PFAM; PF00047; 19.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 12740 MW; 745D103A CRC32;

Query Match 58.1%; Score 471; DB 4; Length 115;
Best Local Similarity 60.0%; Pred. No. 1.03e-82;
Matches 66; Conservative 23; Mismatches 20; Indels 1; Gaps 1;

Db 4 LTQSPDLAVSLGERATINCKSSQTVFYNSKNKYLAQYRKSGOSPELLISWASTRESG 63
QY 4 MTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKLESG 62
DB 64 VPDRFGSGGTDFTLTISLQAEDVAVYVCQYQYNNVPTFGPGTKVDIK 113
QY 63 VPDRFGSGGTDFTLKISGVEAEDGVYYCMQFTHYPFTGGTGLEIK 112

RESULT 10 PRELIMINARY; PRT; 131 AA.

ID Q99671 AC Q99671
DT 01-MAY-1997 (TREMBREL. 03, CREATED)
DT 01-MAY-1997 (TREMBREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA RIU C.J., JIN B.R., CHUNG H.K., HONG H.J.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U66190; G1778126;
DR PFAM; PF00047; 19.
KW SIGNAL.
FT SIGNAL.
FT CHAIN 1 22 POTENTIAL.
FT NON_TER 23 >131 MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE REGION.

RC STRAIN-BALB/C; TISSUE-LIVER;
RX MEDLINE; 87110625.
RA CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;
RL J. IMMUNOL. 138:932-939(1987).
DR EMBL; D00081; D1000494;
FT NON_TER 119
SQ SEQUENCE 119 AA; 13117 MW; C201F8D8 CRC32;

Query Match 62.3%; Score 505; DB 11; Length 119;
Best Local Similarity 75.0%; Pred. No. 9.46e-91;
Matches 75; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Db 20 DVLMQTPLSPVSLGQASISCRSSOSIVHSNGNTLVLYLKPGOSPQLLIYKVSNR 79
QY 1 DVMTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKLE 60
DB 80 SGVPDFRFGSGGTDFTLKISGVEAEDGVYYICMFTHP 119
QY 61 SGVPDFRFGSGGTDFTLKISGVEAEDGVYYICMFTHP 100

RESULT 7 PRELIMINARY; PRT; 119 AA.

ID Q55117 AC Q55117
DT 01-JUN-1998 (TREMBREL. 06, CREATED)
DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C; TISSUE-LIVER;
RX MEDLINE; 87110625.
RA CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;
RL J. IMMUNOL. 138:932-939(1987).
DR EMBL; D00082; D1000495;
FT NON_TER 119
SQ SEQUENCE 119 AA; 13117 MW; 7D3761A1 CRC32;

Query Match 62.0%; Score 502; DB 11; Length 119;
Best Local Similarity 76.0%; Pred. No. 4.86e-90;
Matches 76; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Db 20 DAVMTQPLSPVSLGQASISCRSSOSLNSGNTYNWLLQRPGSQPQLIYKVSNR 79
QY 1 DVMTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKLE 60
DB 80 SGVLDPRFGSGGTDFTLKISRVAEADGLVYFCIQVTHP 119
QY 61 SGVPDFRFGSGGTDFTLKISGVEAEDGVYYICMFTHP 100

RESULT 8 PRELIMINARY; PRT; 133 AA.

ID Q61551 AC Q61551
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DE CC49 FAB PRECURSOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RP SEQUENCE FROM N.A.
RA ABERGEL C., PADLAN E.A., KASHMIRI S.V.S., MILENIC D., CALVO B.,
SCHLOW J.;
RL SUBMITTED (JUN-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; M95574; G193215;
DR PFAM; PF00047; 19.
KW SIGNAL.
FT SIGNAL.
FT SIGNAL.

FT CHAIN 21 >133 CC49 FAB.
SQ SEQUENCE 133 AA; 14528 MW; F1EA6B5F CRC32;
Query Match 61.9%; Score 501; DB 11; Length 133;
Best Local Similarity 61.9%; Pred. No. 8.39e-90;
Matches 70; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Db 21 DIVMQSPSSLPVSGEKVTLSCKSSQSLYSNOKNYLAQYQQKPGQPKLLIYWASAR 80
QY 1 DVMTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKL 59
DB 81 ESGVDPFRFGSGGTDFTLISVKTEDLVAYYCQYYSYPITFGAGTKLVK 133
QY 60 ESGVDPFRFGSGGTDFTLKISGVEAEDGVYYICMFTHTPTFGGKTLEIK 112

RESULT 9 PRELIMINARY; PRT; 115 AA.

ID Q99826 AC Q99826
DT 01-MAY-1997 (TREMBREL. 03, CREATED)
DT 01-MAY-1997 (TREMBREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE ANTI-HIV-1 GP120 V3 LOOP ANTIBODY DOI42-10 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; PRIMATES.
RP SEQUENCE FROM N.A.
RA DITZEL H.J., PARREN P.W.H.I., BINLEY J.M., SODROSKI J., MOORE J.P.,
BARBAS C.F., BURTON D.R.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U82962; G1800287;
DR PFAM; PF00047; 19.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 12740 MW; 745D103A CRC32;

Query Match 58.1%; Score 471; DB 4; Length 115;
Best Local Similarity 60.0%; Pred. No. 1.03e-82;
Matches 66; Conservative 23; Mismatches 20; Indels 1; Gaps 1;

Db 4 LTQSPDLAVSLGERATINCKSSQTVFYNSKNKYLAQYRKSGOSPELLISWASTRESG 63
QY 4 MTQSPFLSVLTIGQPASISCRSSQSLLHSGSNTYNWLLQRPGSQPQLIYLSKLESG 62
DB 64 VPDRFGSGGTDFTLTISLQAEDVAVYCYQYNNVPTFGPGTKVDIK 113
QY 63 VPDRFGSGGTDFTLKISGVEAEDGVYYICMFTHTPTFGGKTLEIK 112

RESULT 10 PRELIMINARY; PRT; 131 AA.

ID Q99671 AC Q99671
DT 01-MAY-1997 (TREMBREL. 03, CREATED)
DT 01-MAY-1997 (TREMBREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; PRIMATES.
RP SEQUENCE FROM N.A.
RA RIU C.J., JIN B.R., CHUNG H.K., HONG H.J.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U66190; G1778126;
DR PFAM; PF00047; 19.
KW SIGNAL.
FT SIGNAL.
FT SIGNAL.

FT CHAIN 1 22 POTENTIAL.
FT CHAIN 23 >131 MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE REGION.
FT NON_TER 131

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Best Local Similarity 55.48; Pred.No. 3.68e-72;
Matches_ 62; Conservative 26; Mismatches 19; Indels 5; Gaps 3;

Db 1 EIVMTQSPATLISPGERATLSRASQS--TS-K--LGWYQQKPGCAPRLLIYGASTRA 55
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy 1 DVMVTQSPPELLVTLGPASISCRSSQLSHSSGNTYLNWLQRPGSQPOLIYLVSKE 60
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 56 TGIPARESGSGSTEFLLTSLSSQSEDFAYYYCQYNMPLTFGGTKVEIK 107
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy 61 SGVPDRFSGSGGTDFLKISGVEAEDGVYYCMQTHYPYTFGGTKLEIK 112
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 13
ID AC OI4535 PRELIMINARY; PRT; 113 AA.
AC OI4535;
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-AUG-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
DE HRV FAB N6-VL (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBL;
RA ITOH K., SUZUKI T.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR.. EMBL: AB006842; D1023041; -.
DR PFAM: PF00047; Ig. 113
FT NON_TER 113
SQ SEQUENCE 113 AA; 12207 MW; A546C704 CRC32;

Query Match 52.18; Score 422; DB 4; Length 113;
Best Local Similarity 58.08; Pred.No. 3.16e-71;
Matches 65; Conservative 20; Mismatches 22; Indels 5; Gaps 2;

Db 3 ELVMTQSPSSLAASVGDRVTTTCRASQSI--SS---YLNWYQQKPKAPKLIIYAASLQ 57
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy 1 DVMTQSPPELVLTLPASISCRSSQLSHSSGNTYLNWLQRPGSQPOLIYLVSKE 60
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 58 SGVPSRFSGSGGTDFLLTSLSSQPEDFATYYCQSYSPITFGQTRLEIK 109
   :|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~
Qy 61 SGVPDRFSGSGGTDFLLKISGVEAEDGVYYCMQTHYPYTFGGTKLEIK 112
   :|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:

RESULT 14
ID AC OI4537 PRELIMINARY; PRT; 115 AA.
AC OI4537;
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-AUG-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
DE HRV FAB N27-VL (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBL;
RA ITOH K., SUZUKI T.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR.. EMBL: AB006844; D1023043; -.
DR PFAM: PF00047; Ig. 115
FT NON_TER 115
SQ SEQUENCE 115 AA; 12417 MW; 96E3C279 CRC32;

Query Match 51.98; Score 420; DB 4; Length 115;
Best Local Similarity 57.58; Pred.No. 9.24e-71;
Matches 65; Conservative 21; Mismatches 22; Indels 5; Gaps 3;

Db ... 3 ELIUTQSPGLISLSPGERATLSRASQSV--SS--SYLAWYQQKPGCAPRLLIYGASSRA 58
   :.:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:
Qy 1 DVMTQSPPELVLTLPASISCRSSQLSHSSGNTYLNWLQRPGSQPOLIYLVSKE 60

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RESULT 15

AC 099514: 100 251

DT 01-MAY-1997 (TREMBLER). 03: IAST SEC

01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)

OS HOMO SAPIENS (HUMAN).

OC EUTHERIA: PRIMATES.

RN [1] SEQUENCE FROM N A
RP

RA HORN M.P., VOGEL M., BIAGGI C., MIESCHER S.M., STADLER B.M.;

DR EMBL; Y08148; E274854; -.

ET NON TER 1

ET	NON_TER	105	105
CO	CORRECTION	105	11303
			04077803
			06000

Best Local Similarity 60.0%: Pred. No. 1.58e-70:

00; conservative 17; mismatches 27; indels 3;

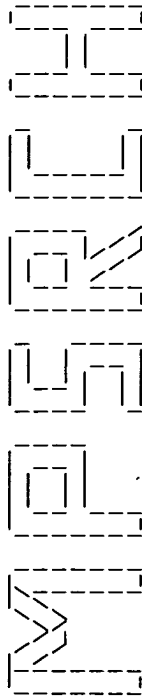
Db 1 VMTQSPSSLSASVGDRTTITCRASQSI--SS--YLNWYQQKPGKAPKLLIYAASLL

QY 3 VMTQSPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSQPLIYLVSKL

db 56 VPSRFGSGSGTDFTLTISSLOPEDEATYYCOOSYSTPVTFGOGTRI.ETK 105

07 63 WDPBESCSCTNFTY YTSUFEAFBNICWVCWAEWHVNVETECWTZT 11

Search completed: Thu Jan 14 17:11:35 1999
Job time : 35 secs.



(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:12:23 1999; MasPar time 7.48 Seconds
Tabular output not generated. 242.407 Million cell updates/sec

Title: >US-08-477-989B-88
Description: (1-112) from US08477989B.pep
Perfect Score: 810
Sequence: 1 DVVMTQSPSPSLVLTGQPAS.....CMQFTHYPYTFQGKLEIK 112

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-genseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 29.850; Variance 154.687; scale 0.193

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	724	89.4	253	11	R59083	Protein encoded from
2	712	87.9	134	11	R59078	LO-CD2a VL and signal
3	638	78.8	272	29	W43913	Mus musculus antibody
4	631	77.9	272	18	W00557	Nematode salivary pro
5	627	77.4	135	24	W24989	Monoclonal antibody 2
6	627	77.4	135	10	W54052	Sequence of the VL re
7	627	77.4	135	20	W01525	Monoclonal antibody 2
8	627	77.4	535	24	W28492	Human p53 protein var
9	627	77.4	535	24	W28491	Human p53 protein var
10	623	76.9	112	5	R24710	Sequence of a chimeri
11	623	76.9	132	5	R24712	Sequence encoded by t
12	622	76.8	113	18	R52057	Light chain variable
13	620	76.5	112	29	W48248	A77 anti-Fc alpha R a
14	618	76.3	132	2	R12361	Light (kappa) chain v
15	614	75.8	131	2	R12239	Mouse MAb 4D12 L cha
16	609	75.2	113	29	W39897	Light chain of the ca
17	608	75.1	141	6	R30454	C242:11 MAb kappa cha
18	608	75.1	141	6	R32541	C242 kappa chain vari

19	605	74.7	133	7	R33951	CTMO1 VL
20	601	74.2	112	29	W40133	Human Mab AB17.1.41 p
21	598	73.8	112	19	R35212	HumB3V1 humanised var
22	598	73.8	114	29	W39805	Variable domain of th
23	597	73.7	113	11	R56652	Anti-CMV monoclonal a
24	596	73.6	110	7	R38159	Sequence of the light
25	595	73.5	112	19	R95218	Human IgM GM607 varia
26	594	73.3	263	3	R15055	Qm212 single chain an
27	593	73.2	112	6	R32239	Humanised MAB light c
28	593	73.2	112	26	W27145	Mature light chain va
29	593	73.2	238	17	R33554	Monoclonal antibody D
30	592	73.1	131	10	R52822	Humanised murine KC-4
31	592	73.1	131	13	R70470	Humanised anti-KC-4 a
32	591	73.0	113	17	R85508	Vlkappa for antibody
33	590	72.8	253	16	R72599	Anti-dansyl single ch
34	589	72.7	239	13	R66757	Anti-tobacco mosaic v
35	588	72.6	238	22	W14937	Murine anti-porcine v
36	588	72.6	238	22	W14942	3F4 Human IgG4 expres
37	586	72.3	114	25	W27544	Human Ab light chain
38	586	72.3	239	5	R24811	Sequence encoded by t
39	586	72.3	281	25	W27560	Consensus single chai
40	585	72.2	112	3	R14393	Modified L3 region of
41	583	72.0	112	3	R14392	L3 region of kappa l1
42	581	71.7	238	10	R55864	4-4-20 VL / 217 / CC4
43	580	71.6	133	25	W29751	Anti-HMFG MAB CTMO1
44	576	71.4	149	20	W03199	Anti-idiotype monoclo
45	576	71.1	241	7	R37645	Sequence of a multiva

ALIGNMENTS

RESULT 1
ID R59083 standard; Protein; 253 AA.
AC R59083;
DE 01-MAY-1995 (first entry)
DE Protein encoded from reading frame 3 of LO-CD2a VL coding region.
KW LO-CD2a; light; heavy; chain; variable; constant; antibody;
KW signal sequence; MRC; vector; hcmv-vlllye-kr-neo; ATCC HB 11423;
KW monoclonal antibody; MAB; T lymphocyte; null cell; B lymphocyte;
KW CD4; CD8; Leu3a; Leu2b; inhibition; immune response; human;
KW T cell; activation; proliferation; inhibition; graft transplantation;
KW graft-versus-host disease; autoimmune disease.
OS Rattus rattus.
FH Key
FT misc_difference 1..253 Location/Qualifiers
FT /note= "X encoded by non-sense codon"
FT misc_difference 20 /note= "Residue not given in the specification"
FT misc_difference 57 /note= "Residue not given in the specification"
FT misc_difference 85 /note= "Residue not given in the specification"
FT misc_difference 112 /note= "Residue not given in the specification"
FT protein /note= "Residue not given in the specification"
FT misc_difference 149..253 /note= "Residues 8..105 of LO-CD2a VL"
FT misc_difference 194 /note= "Residue not given in the specification"

WO9420619-A.
15-SEP-1994.
04-MAR-1994; IB0043.
05-MAR-1993; US-027008.
09-SEP-1993; US-119032.
(UVA) UNIV CATHOLIQUE LOUVAIN.
PI Bazin H, Latienne D;
DR WPI; 94-303026/37.
DR N-PSDB; Q71876.
PT New anti-CD2 monoclonal antibody - used for inhibiting an immune
PT response mediated by T cell activation and proliferation
PT Claim 31; Fig 29B; 10pp; English.
CC The sequences given in R59081-83 represent the protein products which
CC are encoded in all three reading frames from a DNA fragment which
CC represents the coding region for the LO-CD2a light chain variable region

CC from the antibody LO-CD2a, and the leader sequence from the LOCD2a gene.
 CC LO-CD2a is produced by the cell line ATCC HB 11423. It is pref. a rat
 CC monoclonal antibody and is produced using CD2. This antibody, or
 CC fragments of it, binds to all T lymphocytes and also to null cells but
 CC not to B lymphocytes. It binds to all CD4 and CD8 positive cells as
 CC defined by Leu3a and Leu2b antibodies respectively. LO-CD2a can be used
 CC for inhibiting an immune response in a human patient, partic. an immune
 CC response mediated by T cell activation and proliferation resulting from
 CC graft transplantation, graft-versus-host disease or autoimmune diseases.
 CC The missing residues are deduced from the DNA sequence given in the
 CC specification.
 SQ Sequence 253 AA;

Query Match 89.4%; Score 724; DB 11; Length 253;
 Best Local Similarity 87.5%; Pred. No. 5.86e-48;
 Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
 Db 142 dvlitqtptllatigqsvsicsrssqslhssgntynllwllqrgtqgspqpllylvskle 201
 QY 1 DVMTQSPSPSLVLTGQPASISCRSSQSLHSSGNTYNLLWLLQRPQSPQPLIYLVSKLE 60
 Db 202 sgvnfhsgsgtdftlkisgveadlgvvyvcmqfthpytfgagtklelk 253
 QY 61 SGVPDRFSGSGTDTFLKISGVEADGVVYVCMQFTHPYTFTFGQGTKEIK 112

RESULT 2
 ID R59078 standard; Protein; 134 AA.

AC R59078;
 DT 27-APR-1995 (first entry)
 DE LO-CD2a VL and signal peptide from MRC vector hcmv-vlyls-kr-neo.
 KW LO-CD2a; light; heavy; chain; variable; constant; antibody;
 KW signal sequence; MRC; vector; hcmv-vlyls-kr-neo; ATCC HB 11423;
 KW monoclonal antibody; Mab; T lymphocyte; null cell; B lymphocyte;
 KW CD4; CD8; Leu3a; Leu2b; inhibition; immune response; human;
 KW T cell; activation; proliferation; graft transplantation;
 KW graft-versus-host disease; autoimmune disease.
 OS Rattus rattus.

Key	Location/Qualifiers
peptide	1..22
protein	/note= "Signal peptide"
FT	23..134
FT	/note= "LO-CD2a VL"
FT	misc_difference 13
FT	/note= "Encoded by CTT"
FT	misc_difference 15
FT	/note= "Encoded by TTT"
FT	misc_difference 93..94
FT	/note= "Encoded by CGGTCA"
FT	misc_difference 103
FT	/note= "Encoded by AGT"
FT	misc_difference 105
FT	/note= "Encoded by CTG"
FT	misc_difference 112
FT	/note= "Encoded by CTT"
FT	misc_difference 128
FT	/note= "Encoded by GGG"

WO9420619-A.
 PD 15-SEP-1994.
 PF 04-MAR-1994; IB0043.
 PR 05-MAR-1993; US-027008.
 PR 09-SEP-1993; US-119032.
 PA (UVLO-) UNIV CATHOLIQUE LOUVAIN.
 PI Bazin H, Latine D;
 DR WPI; 94-303026/37.
 DR N-PSDB; Q71875.
 DR New anti-CD2 monoclonal antibody - used for inhibiting an immune
 PT response mediated by T cell activation and proliferation
 PS Claim 29; Fig 29A; 101pp; English.
 CC This sequence represents the LO-CD2a light chain variable region from
 CC the antibody LO-CD2a, and the signal sequence from the MRC vector hcmv-
 CC vlyls-kr-neo. LO-CD2a is produced by the cell line ATCC HB 11423. It
 CC is pref. a rat monoclonal antibody and is produced using CD2. This

CC antibody, or fragments of it, binds to all T lymphocytes and also to
 CC null cells but not to B lymphocytes. It binds to all CD4 and CD8.
 CC positive cells as defined by Leu3a and Leu2b antibodies respectively.
 CC LO-CD2a can be used for inhibiting an immune response in a human
 CC patient, partic. an immune response mediated by T cell activation
 CC and proliferation resulting from graft transplantation, graft-versus-
 CC host disease or autoimmune diseases.
 SQ Sequence 134 AA;

Query Match 87.9%; Score 712; DB 11; Length 134;
 Best Local Similarity 85.7%; Pred. No. 5.49e-47;
 Matches 96; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 23 dqltqspptllatigqsvsicsrssqslhssgntynllwllqrgtqgspqpllylvskle 82
 QY 1 DVMTQSPSPSLVLTGQPASISCRSSQSLHSSGNTYNLLWLLQRPQSPQPLIYLVSKLE 60
 Db 83 sgvnfhsgsgtdftlkisgveadlgvvyvcmqfthpytfgagtklelk 134
 QY 61 SGVPDRFSGSGTDTFLKISGVEADGVVYVCMQFTHPYTFTFGQGTKEIK 112

RESULT 3
 ID W43913 standard; Protein; 272 AA.

AC W43913;
 DT 17-JUN-1998 (first entry)
 DE Mus musculus antibody specific for cyst nematode salivary protein.
 KW Cellulase activity; nematode; crop protection; parasitic;
 KW subventral oesophageal protein; cyst nematode;
 KW salivary protein.
 OS Mus musculus.

Key	Location/Qualifiers
Domain	1..112
FT	/note= "antibody variable domain light chain"
FT	25..39
FT	/note= "Complementarity Determining Region"
FT	55..61
FT	/note= "Complementarity Determining Region"
FT	93..102
FT	/note= "Complementarity Determining Region"
FT	113..127
FT	/note= "Gly-Ser peptide linker"
FT	128..273
FT	/note= "antibody variable domain heavy chain"
FT	158..162
FT	/note= "Complementarity Determining Region"
FT	529..579
FT	/note= "Complementarity Determining Region"
FT	226..232
FT	/note= "Complementarity Determining Region"

EP-818538-A1.
 PD 14-JAN-1998.
 PF 08-JUL-1996; 201890.
 PR 08-JUL-1996; EP-201890.
 PA (RIJK-) RIJSLANDBOUWUNIVERSITEIT WAGENINGEN.
 PI Bakker J, De Boer JM, Gommers FJ, Govers A, Helder J,
 PI Roosien J, Schots A, Schouten A, Smant G, Stiekema WJ,
 PI Stokermans JFW;
 DR WPI; 98-065307/07.
 DR N-PSDB; T86646.
 DR Nematodal cellulase peptide(s) - useful as industrial cellulolytic
 PT enzymes or for plant protection
 PS Example; Pages 22-24; 28pp; English.
 CC The sequence is that encoding a peptide fragment of an antibody
 CC specific for a salivary protein of cyst nematodes. It can be used
 CC to help protect plants against parasitic nematodes.
 SQ Sequence 272 AA;

Query Match 78.8%; Score 638; DB 29; Length 272;
 Best Local Similarity 81.3%; Pred. No. 5.20e-41;
 Matches 91; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Db 1 dvmtqtptllatigqsvsicsrssqslhssgntynllwllqrgtqgspqpllylvskle 60

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QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRRGSGPQPLIYLVSKLE 60
Db 61 sgvpdrftgsgsgtdftlkisrveavdlgyvycwqgthlpytfgggtkklk 112
QY 61 SGVPDRFSGSGGTDFTLKISGVEAEADVGYVYCMQFTHYPTFGQGTKEIK 112

RESULT 4
ID W00557 standard; Protein; 272 AA.
AC W00557;
DE Nematoe salivary protein antibody construct.
KW Cyst nematode; salivary protein; svp49; transgenic plant;
KW Biological control; crop protection; antibody engineering;
KW Heterodera; Globodera; Punctodera; monoclonal antibody.
OS Mus musculus.
FH Key
FT domain 1..112 Location/Qualifiers
FT /label= Light_chain_variable_domain
FT /region 25..39
FT /label= CDR
FT /region 55..61
FT /label= CDR
FT /region 94..102
FT /label= CDR
FT /region 113..127
FT /label= Gly-Ser_linker
FT /region 128..272
FT /label= Heavy_chain_variable_domain
FT /region 158..162
FT /label= CDR
FT /region 177..193
FT /label= CDR
FT /region 226..232
FT /label= CDR
FN W09622372-A2.
PD 25-JUL-1996.
PE 17-JAN-1996; NL0033.
PR 17-JAN-1995; EP-200110.
PA (RIJK-) RIJSLANDBOUWOGESCHOOL WAGENINGEN.
PI Bakker J, Schots A, Stiekema WJ;
DR WPI; 96-354529/35.
DR N-PSDB; T35691.
PT Antibody against stage two juvenile nematode salivary proteins
PT used in the production of transgenic plants, resistant to nematode
PT infection
PT Claim 7; Page 17-19; 25pp; English.
CC An engineered antibody construct (W00557) comprises the 2 variable
CC regions of an antibody that specifically reacts with a salivary
CC protein of cyst nematodes, fused by a 15-mer linker peptide. The
CC antibody is pref. mouse monoclonal antibody MGR48, which recognises
CC subunita1 oesophageal proteins svp30, svp31a, svp31b, svp32, svp39
CC and svp49 (see also W00556) of cyst nematode second stage juveniles
CC (J2), and which was raised using J2 protein fractions of Globodera
CC rostochiensis. Transgenic plants expressing such antibody
CC constructs are protected against attack from Heterodera, Punctodera
CC and Globodera cyst nematodes.
CC Sequence 272 AA;

Query Match 77.9%; Score 631; DB 18; Length 272;
Best Local Similarity 80.4%; Pred. No. 1.91e-40;
Matches 90; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Db 1 dvvmtqtpslvtlgtqcpasiscskssqllhsdgktylswfsgrpgskrllylvskld 60
QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRRGSGPQPLIYLVSKLE 60
Db 61 sgvpdrftgsgsgtdftlkisrveavdlgyvycwqgthlpytfgggtkklk 112
QY 61 SGVPDRFSGSGGTDFTLKISGVEAEADVGYVYCMQFTHYPTFGQGTKEIK 112

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RESULT 5
ID W24989 standard; Protein; 135 AA.
AC W24989;
DE Monoclonal antibody ZM1-1 VI region.
KW Heavy chain; light chain; variable region; human; monoclonal antibody;
KW Immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogeneic;
KW peripheral blood lymphocyte; surface antigen; cell culture; ion exchange;
KW chromatography; size separation; primer; PCR; polymerase chain reaction;
KW amplification; hybridoma; infection; immunosuppression; hepatitis;
KW liver transplant.
OS Homo sapiens.
FH Key
FT peptide 1..122 Location/Qualifiers
FT /note= "leader sequence"
FT /protein 23..135
FT /note= "mature protein"
FT /region 23..122
FT /note= "VkII region"
FT /domain 46..62
FT /note= "complementarity determining region 1"
FT /domain 77..83
FT /note= "complementarity determining region 2"
FT /domain 116..124
FT /note= "complementarity determining region 3"
FT /region 123..135
FT /note= "Jx5 region"
FN US5648077-A.
PD 15-JUL-1997.
PE 05-SEP-1986; 904517.
PR 21-APR-1992; US-871426.
PR 05-SEP-1986; US-904517.
PR 31-OCT-1986; US-925196.
PR 11-MAY-1988; US-192754.
PR 15-JUN-1990; US-538796.
PR 27-MAR-1991; US-676036.
PR 14-JUN-1994; US-259372.
PR 06-JUN-1995; US-468671.
PA (SANO ) SANDOZ LTD.
PI Ostberg LG;
DR WPI; 97-372021/34.
DR N-PSDB; T85843.
PT Treatment of hepatitis B - with human monoclonal antibody
PS Example 8; Column 21-22; 25pp; English.
CC This is the amino acid sequence of the light chain variable (VL) region
CC from the human monoclonal antibody (MAB) ZM1-1. The MAB was generated
CC by immunising humans with a hepatitis B virus (HBV) vaccine, isolating
CC peripheral blood lymphocytes (PBL) and fusing them with a mouse/human
CC xenogeneic cell line SP2-4. 5 cell lines were isolated: PE1-1, ZM1-1,
CC ZM1-2, MD3-4 and LQ3-3. The cell lines were then tested for production
CC of an anti-hepatitis B virus surface antigen antibody by ELISA. The MABs
CC are then purified from large scale cell culture by protein A
CC chromatography, size separation on Sephacryl S300 gel and ion exchange
CC chromatography on Q-Sepharose. The heavy and light chains of the MABs
CC were isolated and their amino acid sequences determined. Primers were
CC generated and used to amplify cDNA synthesised from RNA purified from
CC each hybridoma cell line. The sequences of the heavy and light chains
CC (nucleic acid and amino acid) from MABs PE1-1, ZM1-1, ZM1-2 and MD3-4 are
CC shown in T85838-45 and W24984-91. The MABs can be used to treat HBV
CC infections in immunosuppressed patients or patients with chronic active
CC hepatitis, especially liver transplant patients.
CC Sequence 135 AA;

Query Match 77.4%; Score 627; DB 24; Length 135;
Best Local Similarity 82.1%; Pred. No. 4.00e-40;
Matches 92; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Db 23 dvvvtqslpvtlgtqcpasiscrsslsldsdgntylwnflgrpgskprlllylvskld 82
QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRRGSGPQPLIYLVSKLE 60
Db 83 sgvpdrftgsgsgtdftlkisrveavdlgyvycwqgthlpytfgggtkklk 134

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QY	61	SGVPDRFSGSGGTDTLTKISGVEAEADVGVYCMQTHPYTFGQGTGLEIK 112
FW	Monoclonal antibody; diagnosis; treatment; infection; hepatitis B; xenogeneic hybridoma; SPAZ 4; PEI-1; ZMI-1; ZMI-2; MD3-4; L03-3; IgG1 class; heavy chain; light chain; variable region.	
OS	Homo sapiens.	
FW	Key	
FW	Location/Qualifiers	
FW	peptide 1..22	
FW	/label= leader_sequence	
FW	region 23..122	
FW	/label= V_Kappa_III_region	
FW	region 23..45	
FW	/label= framework_region	
FW	region 46..62	
FW	/label= CDR1	
FW	region 63..76	
FW	/label= framework_region	
FW	region 77..83	
FW	/label= CDR2	
FW	region 84..115	
FW	/label= Framework_region	
FW	region 116..124	
FW	/label= CDR3	
FW	region 123..135	
FW	/label= J_Kappa_5 region	
FW	US555354-A.	
FW	PN 15-OCT-1996.	
FW	PF 05-SEP-1986; 904517.	
FW	PR 05-SEP-1986; US-904517.	
FW	PR 31-OCT-1986; US-925196.	
FW	PR 11-MAY-1988; US-192754.	
FW	PR 15-JUN-1990; US-538796.	
FW	PR 27-MAR-1991; US-676036.	
FW	PR 21-APR-1992; US-871426.	
FW	PR 14-JUN-1994; US-259372.	
FW	PA (SANO) SANDOZ LTD.	
FW	PI Ostberg LG;	
FW	DR WPI; 96-476304/47.	
FW	DR N-PSDB; T46131.	
FW	PT Human monoclonal antibodies specific for hepatitis B surface antigen - are used to treat or prevent infection or in diagnostic assays	
FW	PS Example 9; Column 39-40; 26pp; English.	
FW	CC Monoclonal antibodies effective for the diagnosis and treatment of diseases caused by infection with hepatitis B have been prepared from a cell line obtained by fusing a xenogeneic hybridoma designated SPAZ 4 with blood cells of a patient immunised with hepatitis B vaccine.	
FW	CC Specific antibodies are PEI-1, ZMI-1, ZMI-2, MD3-4 and L03-3, each of these being of the IgG1 class. The present sequence is the light variable chain of ZMI-1.	
FW	CC Sequence 135 AA;	
FW	SQ	
FW	Query Match 77.4%; Score 627; DB 20; Length 135;	
FW	Best Local Similarity 82.1%; Pred. No. 4.00e-40;	
FW	Matches 92; Conservative 7; Mismatches 13; Indels 0; Gaps 0;	
DB	23 dvvtqtspslpvtlqgpasiscrslslvdsdgnlynlwflqrpqgsprllyqlssrd 82	
QY	1 DVVMTQSPPSLLVTLGQPASISCRSSQLSHSSGNTYLNWLLQRPQSQPQPILYLSKLE 60	
DB	83 sgvpdrfsgsgsgtdftlkisrveaedvgvycmqgthwptifggqtrleik 134	
QY	61 SGVPDRFSGSGGTDTLTKISGVEAEADVGVYCMQTHPYTFGQGTGLEIK 112	
FW	Key	
FW	Location/Qualifiers	
FW	peptide 1..22	
FW	/label= leader	
FW	region 23..122	
FW	/label= VL II	
FW	region 46..62	
FW	/label= CDR 1	
FW	region 77..83	
FW	/label= CDR 2	
FW	region 116..124	
FW	/label= CDR 3	
FW	region 123..135	
FW	/label= JL 5	
FW	WO9411495-A.	
FW	PN 26-MAY-1994.	
FW	PF 06-NOV-1992; UO9749.	
FW	PR 06-NOV-1992; WO-UO9749.	
FW	PA (SANO) SANDOZ LTD.	
FW	PI Ostberg LG;	
FW	DR WPI; 94-183497/22.	
FW	DR N-PSDB; Q64055.	
FW	PT Monoclonal antibodies active against Hepatitis B surface antigen - for diagnosis and treatment of Hepatitis B virus	
FW	PS Example; Page 41; 53pp; English.	
FW	CC Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZMI-2, ZMI-1 and PEI-1 hybridoma cell lines were derived from lymphocytes of individuals immunised with Heptavax (Merck & Co).	
FW	CC Antibodies PEI-1, ZMI-1, M21-2 and MD3-4 belong to the IgG1 class.	
FW	CC The cell lines producing PEI-1, ZMI-1 and ZMI-2 were deposited as ATCC HB234, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable (LH) chains of Abs PEI-1, ZMI-1, ZMI-2 and MD3-4 were isolated and sequenced. Total RNA was extracted from 10(7) hybridoma cells of each cell line. ss DNA was synthesised using AMV-reverse transcriptase and oligo-dt as primer. PCRs were performed and amplified DNA was size selected. ss DNA for sequencing was isolated from each positive clone after superinfection with M13K07.	
FW	CC Sequencing was by the dideoxy chain termination method (Sanger et al.).	
FW	CC Sequence 135 AA;	
FW	SQ	
FW	Query Match 77.4%; Score 627; DB 10; Length 135;	
FW	Best Local Similarity 82.1%; Pred. No. 4.00e-40;	
FW	Matches 92; Conservative 7; Mismatches 13; Indels 0; Gaps 0;	
DB	23 dvvtqtspslpvtlqgpasiscrslslvdsdgnlynlwflqrpqgsprllyqlssrd 82	
QY	1 DVVMTQSPPSLLVTLGQPASISCRSSQLSHSSGNTYLNWLLQRPQSQPQPILYLSKLE 60	
DB	83 sgvpdrfsgsgsgtdftlkisrveaedvgvycmqgthwptifggqtrleik 134	
QY	61 SGVPDRFSGSGGTDTLTKISGVEAEADVGVYCMQTHPYTFGQGTGLEIK 112	
FW	Key	
FW	Location/Qualifiers	
FW	peptide 1..22	
FW	/label= leader	
FW	region 23..122	
FW	/label= VL II	
FW	region 46..62	
FW	/label= CDR 1	
FW	region 77..83	
FW	/label= CDR 2	
FW	region 116..124	
FW	/label= CDR 3	
FW	region 123..135	
FW	/label= JL 5	
FW	WO9411495-A.	
FW	PN 26-MAY-1994.	
FW	PF 06-NOV-1992; UO9749.	
FW	PR 06-NOV-1992; WO-UO9749.	
FW	PA (SANO) SANDOZ LTD.	
FW	PI Ostberg LG;	
FW	DR WPI; 94-183497/22.	
FW	DR N-PSDB; Q64055.	
FW	PT Monoclonal antibodies active against Hepatitis B surface antigen - for diagnosis and treatment of Hepatitis B virus	
FW	PS Example; Page 41; 53pp; English.	
FW	CC Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZMI-2, ZMI-1 and PEI-1 hybridoma cell lines were derived from lymphocytes of individuals immunised with Heptavax (Merck & Co).	
FW	CC Antibodies PEI-1, ZMI-1, M21-2 and MD3-4 belong to the IgG1 class.	
FW	CC The cell lines producing PEI-1, ZMI-1 and ZMI-2 were deposited as ATCC HB234, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable (LH) chains of Abs PEI-1, ZMI-1, ZMI-2 and MD3-4 were isolated and sequenced. Total RNA was extracted from 10(7) hybridoma cells of each cell line. ss DNA was synthesised using AMV-reverse transcriptase and oligo-dt as primer. PCRs were performed and amplified DNA was size selected. ss DNA for sequencing was isolated from each positive clone after superinfection with M13K07.	
FW	CC Sequencing was by the dideoxy chain termination method (Sanger et al.).	
FW	CC Sequence 135 AA;	
FW	SQ	

QY	61	SGVPDRFSGSGSTDTFLKISGVEAEADVGVVYCMQTHTPYTFGGQTKLEIK	112
RESULT			
ID	R54052	standard; Protein; 135 AA.	
AC	R54052;		
DT	08-NOV-1994	(first entry)	
DE	Sequence of the VL region of monoclonal antibody ZM1-1 against Hepatitis B virus surface antigen.		
KW	Hepatitis B virus; surface antigen; monoclonal antibody; therapy;		
KB	HBsAg; diagnosis; HBV.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	region	1..22	
FT	region	/label= leader	
FT	region	23..122	
FT	region	/label= VL II	
FT	region	46..62	
FT	region	/label= CDR 1	
FT	region	77..83	
FT	region	/label= CDR 2	
FT	region	116..124	
FT	region	/label= CDR 3	
FT	region	123..135	
FT	region	/label= JL 5	
FT	WO9411495-A.		
PD	26-MAY-1994.		
PF	06-NOV-1992; UO9749.		
PR	06-NOV-1992; WO-UO9749.		
PA	(SANO) SANDOZ LTD.		
PI	Ostberg LG;		
PT	WPI; 94-183497/22.		
DR	N-PSDB; Q64055.		
PT	Monoclonal antibodies active against Hepatitis B surface antigen - for diagnosis and treatment of Hepatitis B virus		
CC	Example; Page 41; 53pp; English.		
CC	Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZM1-2, ZM1-1 and PEI-1 hybridoma cell lines were derived from lymphocytes of individuals immunised with Heptavax (Merck & Co).		
CC	Antibodies PEI-1, ZM1-1, M21-2 and MD3-4 belong to the IgG1 class.		
CC	The cell lines producing PEI-1, ZM1-1 and ZM1-2 were deposited as ATCC HB234, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable (LH) chains of Abs PEI-1, ZM1-1, ZM1-2 and MD3-4 were isolated and sequenced. Total RNA was extracted from 10(7) hybridoma cells of each cell line. ss DNA was synthesised using AMV-reverse transcriptase and oligo-dT as primer. PCRs were performed and amplified DNA was size selected. ss DNA for sequencing was isolated from each positive clone after superinfection with M13k07.		
CC	Sequencing was by the dideoxy chain termination method (Sanger et al.).		
CC	Sequence	135 AA;	
SQ			
Query Match 77.4%; Score 627; DB 10; Length 135; Best Local Similarity 82.1%; Pred. No. 4.00e-40; Matches 92; Conservative 7; Mismatches 13; Indels 0; Gaps 0;			
Db	23	dvvvtgspislpvltlqgpasiscrslsvdsdgnlynlwflqrpgsqprlllyqlssrd	82
QY	1	DVVMTPSPPELVLTGLQPASISCRSSQLSHSSGNLYNLWLQRPGSQPQPLIYLSKLE	60
Db	83	sgvpdrfsgsggstddftlklsrveaedvgvyvmqgthwpitfgggtrleik	134
QY	61	SGVPDRFSGSGSTDTFLKISGVEAEADVGVVYCMQTHTPYTFGGQTKLEIK	112
RESULT			
ID	W01525	standard; Protein; 135 AA.	
AC	W01525;		
DT	04-MAR-1997	(first entry)	
DE	Monoclonal antibody ZM1-1 light chain variable region.		

Claim 36; Pages 88-90; 133pp; French.
CC Claimed variants of protein .p53 have at least part of the
CC oligomerisation domain deleted and replaced by a leucine zipper
CC domain. The mutants preferably also have at least part of the p53
CC transactivation domain (amino acids 1-74) deleted and replaced by
CC the transactivating domain (TD) from herpes simplex virus viral
CC protein VP16 (amino acids 411-490) or by a protein domain able to
CC bind selectively to a transactivator, especially a single-chain
CC antibody variable domain (scFv). The present sequence is that of
CC a specifically claimed p53 variant designated S-325 and comprising
CC a scFv domain, amino acids 75-325 of human wild-type p53 and a
CC leucine zipper domain at the C-terminal. The p53 variants are
CC more active and more stable tumour suppressors and apoptosis-inducing
CC agents than wild-type p53 and are active where the wild-type protein
CC is not, i.e. they are not inactivated by dominant negative or oncogenic
CC mutants, nor by other cellular proteins (because the leucine zipper
CC domain prevents formation of inactive mixed oligomers).
SQ Sequence 535 AA;

Query Match 77.4%; Score 627; DB 24; Length 535;
--Best Local Similarity --79.5%; Pred. No. 4.00e+40;
Matches 89; Conservative 11; Mismatches 12; Indels 0; Gaps 0

Dbb 134 dvlmtdptltlsvtlgqpassiscksgslsdgktylnwllqrpgsqkrlylvskld 193
QY :|::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
1 DVMVTGSPSLLVTLGPASISCRSSQLSHSGSNLYNLWLLQRPGSQPQLYLVSKLE 60

Dbb 194 sgvpdrftsgsggtfdtklnrveaedlgvyycwgqthsppltfgagtklelk 245
QY :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
61 SGVPDRFGSGSGGTDTLTKISGVEADVGYYCMQTHTPYTFQGQTKLEIK 112

RESULT 10

ID R24710 standard; Protein; 112 AA.

AC R24710;

DE 28-DEC-1992 (first entry)

DT Sequence of a chimeric anti-human fibrin antibody light chain

DE variable region contg. complementarity determining regions (CDRs)

DE A, B and C.

DE Chimeric monoclonal antibody; anti-fibrin antibody;

KW antithrombotic agent; myocardial infarction therapy.

OS Synthetic.

FH Key Location/Qualifiers

FT region 24..39 /label= CDR A

FT region 55..61 /label= CDR B

FT region 94..101 /label= CDR C

FT EP-491351-A.

PN 17-JUN-1992.

PD 24-JUN-1992.

PP 18-DEC-1991; 121591.

PR 18-DEC-1990; JP-413829.

PR 11-NOV-1991; JP-294464.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Iwasa S, Taka H, Watanabe T, Tada H;

DR WPI; 92-208528/26.

PT Chimeric monoclonal antibodies - contain anti-human fibrin

PT antibody light and heavy chain variable and constant for treating

PT thrombotic conditions e.g. myocardial infarction

PS Disclosure; Page 8; 87pp; English.

CC The inventors claim a chimeric monoclonal antibody which contains an

CC anti-human fibrin antibody light chain variable region contg. at

CC least one of the polypeptide chains A, B and C (R24704, R24705, R24706)

CC and a human antibody light chain constant region. A pref'd. chimeric

CC monoclonal antibody contains all three complementarity determining

CC regions. The chimeric Abs can be used both in vivo and in vitro

CC and, since they have very low immunogenicity as compared with mouse

CC Abs, they can be administered to humans for diagnostic and

CC therapeutic purposes. They are also more stable and show a longer

CC half-life in the blood as compared with the original mouse Abs.

SQ Sequence 112 AA;

QY 61 SGVPRFSGSGGDTFTLKISGVEADVGVYCMQFTHPYTFGQGTKLEIK 112

RESULT 12

ID	R52057 standard; Protein; 113 AA.
AC	R52057;
DE	10-OCT-1996 (first entry)
DT	Light chain variable region of human KV2F antibody.
DE	antibody; humanised; murine; human; heavy chain; light; variable;
KW	framework region; complementarity determining region; reshaping;
KW	modelling; surface residue; modify.
KW	Homo sapiens.
OS	Homo sapiens.
FH	Key
FT	Location/Qualifiers
FT	1..23
FT	/label= framework_region_1
FT	/note= "FR 1"
FT	24..39
FT	/label= complementarity_determining_region_1
FT	/note= "CDR 1"
FT	40..54
FT	/note= "FR 2"
FT	55..61
FT	/note= "CDR 2"
FT	62..95
FT	/note= "FR 3"
FT	96..105
FT	/note= "CDR 3"
PN	EP-592106-A1.
PD	13-APR-1994.
PF	07-SEP-1993; 307051.
PR	09-SEP-1992; US-942245.
PA	(PEDE/) PEDERSEN J T.
PA	(IMMU-) IMMUNOGEN INC.
PI	Gulid BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
DR	WPI; 94-120230/15.
PT	Method of resurfacing of rodent antibodies to produce humanised
PT	antibody forms - for producing non-human antibodies with improved
PT	therapeutic efficiency by presenting human surface on V-region
PT	Example 1; Fig 4A; 230pp; English.
PT	Modification of a rodent antibody (Ab) or fragment by resurfacing in
PT	order to produce a humanised rodent Ab can be determined by calculating
PT	homology between murine and human Ab antibody surfaces. In order to test
PT	the resurfacing approach of the invention, three humanisation experiments
PT	were set up: (1) traditional loop grafting; (2) resurfacing approach
PT	using most similar chain; and (3) resurfacing approach using human
PT	sequences with most similar surface residues. The Ab used was the murine
PT	anti-N901 Ab (see R52055). Experiment 2 was carried out using the murine
PT	sequence which represents the human KV2F Ab light chain variable region
PT	with 87 percent homology with anti-N901 Ab. N901/KV2F (R52058) was prepd.
PT	by CDR grafting.
PT	Sequence 113 AA;
SQL	

Query Match 76.8%; Score 622; DB 18; Length 113;
Best Local Similarity 82.3%; Pred. No. 1.01e-39;
Matches 93; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Db	1 dvmtqslslpvtlqgpasiscrsagelydsdntlynlvqfqrpgsgprllykvsnr 60
QY	1 DVMVTQSPSLVLTIGQPASISCRSSGSLSSHTSSGTYLNLQRPQSGPQPLVLSKLE 60
Db	61 sgvpdrfsgsgsgtdftlkisrrveaedgvyycmqgthswtfggqtkveik 113
QY	61 SGVPRFSGSGGDTFTLKISG-VEADVGVYCMQFTHPYTFGQGTKLEIK 112

RESULT 13

ID	W48248 standard; Protein; 112 AA.
AC	W48248;
DT	22-JUN-1998 (first entry)
DE	A77 anti-Fc alpha R antibody light chain variable V kappa region.
KW	A77 anti-Fc alpha R antibody; Fc-alpha receptor; antigen; cancer;
KW	cytotoxic; white blood cell; infection.
OS	Synthetic.

OS Homo sapiens.
 PN WO9802463-A1.
 PD 22-JAN-1998.
 PF 10-JUL-1997; U12013.
 PR 11-JUL-1996; US-678194.
 PA (MEDA-) MEDAREX INC.
 PI Deo YM, Graziano R, Keler T;
 DR WPI: 98-110533/10.
 DR N-PSDB; V20601.
 PT Multispecific binding molecules reactive with Fc-alpha receptor and
 antigen - for treatment and prevention of cancer and infections by
 activating cytotoxic potential of Fc-alpha on white blood cells
 Claim 18: Page 60; 106pp; English.
 PS The present sequence represents A77 anti-Fc alpha R antibody light chain
 variable V kappa region, which is used to produce the humanised
 determinant in a bi-specific binding molecule of the present invention.
 CC The present invention describes a bi- or multi-specific binding molecule
 (I) comprising a first binding determinant (BD1) which binds a Fc alpha
 receptor and a second BD (BD2) that binds to at least one antigen (Ag).
 CC (I) are used: (i) to eliminate/reduce unwanted cells in a subject (human
 or animal); (ii) to vaccinate against pathogens (specifically Candida
 but many others disclosed including hepatitis and human immune
 deficiency viruses); (iii) to arm effector cells against pathogens or
 cancer cells. Ag may also be an allergen. (I) exploits the cytotoxic
 (cytolytic and phagocytic) potential of Fc alpha on white blood cells,
 CC improving their on cancer/infected cells. When used in vaccines, (I) may
 CC reduce the amount of antigen needed, and may be effective in patients
 CC who do not respond well to antigen.
 SQ Sequence 112 AA;

Query Match 76.58; Score 620; DB 29; Length 112;
 Best Local Similarity 77.78; Pred. No. 1.47e-39;
 Matches 87; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
 Db 1 digitqspstltitgqpsafckssgllsdgktnlwnllqrggspkrllylvskld 60
 QY 1 DVVMTQSPPLSLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60
 Db 61 sgvpdrftgsgsgtdftlkisrveaedlgyvycwqgshfptfgagtklel 112
 QY 61 SGVPDRFSGSGGTDFTLKISGVEADGVYVYCMQFTHYPTFGGQTKLEIK 112

RESULT 14
 ID R12361 standard; Protein; 132 AA.
 AC R12361;
 DT 15-AUG-1991 (first entry)
 DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.
 KW Chimeric antibodies; immunocjugates; HIV; AIDS.
 OS Mus musculus.
 PN WO9107493-A.
 PD 30-MAY-1991.
 PF 13-NOV-1990; U06615.
 PR 13-NOV-1989; US-433730.
 PA (XOMA-) XOMA CORP.
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
 DR WPI: 91-178044/24.
 DR N-PSDB; Q12063.
 PT New chimeric mouse-human antibodies - used to detect, kill and
 remove HIV-1 antigen from sample
 PS Disclosure; fig 18; 107pp; English.
 CC This is the light (kappa) - chain variable (V) region of a mouse
 CC monoclonal antibody (MAB), 4D12, and is specific for an HIV-1
 CC viral antigen. It is used in the construction of a chimeric
 CC MAB comprising heavy and light chains having murine V regions
 CC and human C regions. The chimeric MABs are more effective than
 CC murine MAB 4D12 since they have an increased compatibility in
 CC humans. The heavy and light chain V-regions are joined by
 CC manipulating their respective joining (J) regions, to generate
 CC restriction enzyme recognition sites. The chimeric MABs can be
 CC used as immunocjugates, in association with e.g. toxins for HIV
 CC treatment. They can also be used in diagnosis of HIV.

CC See also Q12056-62.
 SQ Sequence 132 AA;
 Query Match 76.38; Score 618; DB 2; Length 132;
 Best Local Similarity 75.9%; Pred. No. 2.12e-39;
 Matches 85; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 Db 21 dvmtqptltitgqpsafckssgllsdgktnlwnllqrggspkrllylvskld 80
 QY 1 DVVMTQSPPLSLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60
 Db 81 sgvpdrftgsgsgtdftlkisrveaedlgyvycwqgshfptfgagtklel 132
 QY 61 SGVPDRFSGSGGTDFTLKISGVEADGVYVYCMQFTHYPTFGGQTKLEIK 112

RESULT 15
 ID R12239 standard; Protein; 131 AA.
 AC R12239;
 DT 19-AUG-1991 (first entry)
 DE Mouse MAB 4D12 L chain V region.
 KW HIV-1; chimera.
 OS Mus sp.
 PN WO9107494-A.
 PD 30-MAY-1991.
 PF 13-NOV-1990; U06627.
 PR 13-NOV-1989; US-433703.
 PA (XOMA-) XOMA CORP.
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
 DR WPI: 91-178106/24.
 DR N-PSDB; Q12019.
 PT New chimeric mouse human antibodies - used in treatment, diagnosis
 PT and prophylaxis of HIV infections.
 PS Disclosure; Fig 18; 108pp; English.
 CC The mouse VL gene product may be used to produce chimeric mouse-
 CC human Abs against HIV-1 comprising human Ig constant regions and
 CC murine variable regions. These novel sequence are useful in
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be
 CC produced by a bacterial, yeast or mammalian expression system.
 SQ Sequence 131 AA;

Query Match 75.88; Score 614; DB 2; Length 131;
 Best Local Similarity 76.6%; Pred. No. 4.45e-39;
 Matches 85; Conservative 15; Mismatches 11; Indels 0; Gaps 0;
 Db 21 dvmtqptltitgqpsafckssgllsdgktnlwnllqrggspkrllylvskld 80
 QY 1 DVVMTQSPPLSLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60
 Db 81 sgvpdrftgsgsgtdftlkisrveaedlgyvycwqgshfptfgagtklel 131
 QY 61 SGVPDRFSGSGGTDFTLKISGVEADGVYVYCMQFTHYPTFGGQTKLEI 111

Search completed: Thu Jan 14 17:12:57 1999
 Job time : 34 secs.

WORLD
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:14:30 1999; Waspar time 8.61 Seconds
Tabular output not generated. 513.206 Million cell updates/sec

Title: >US-08-477-989B-93
Description: (1-118) from US08477989B.pep
Perfect Score: 856
Sequence: 1 QVQLVQSGAEVKRPGASVKV.....GKFNRYFAYWGQGLTVTVSS 118

Scoring table: PAM 150
Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r58
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 41.723; Variance 109.046; scale 0.383

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	655	76.5	118	2	S36265 Ig heavy chain V regi	1.20e-80
2	653	76.3	135	2	S49530 anti-Sm antibody VH c	2.46e-80
3	613	71.6	123	2	D33548 Ig heavy chain V-1 re	4.25e-74
4	592	69.2	116	2	S55342 Ig heavy chain V regi	7.80e-71
5	584	68.2	121	2	S20783 Ig heavy chain V regi	1.36e-69
6	583	68.1	138	2	S21810 Ig heavy chain V regi	1.94e-69
7	582	68.0	246	2	S38950 Ig gamma chain - mous	2.78e-69
8	582	68.0	446	2	S40295 Ig gamma-2a chain (ma	2.78e-69
9	582	68.0	474	2	S25057 Ig gamma-2b chain - m	2.78e-69
10	581	67.9	110	2	PH1869 Ig heavy chain V regi	3.97e-69
11	581	67.9	118	2	C30360 Ig heavy chain V regi	3.97e-69
12	580	67.8	136	2	S31600 Ig heavy chain V regi	5.67e-69
13	579	67.6	120	2	PH0962 Ig heavy chain V regi	8.10e-69
14	577	67.4	120	2	B22769 Ig heavy chain V regi	1.65e-68
15	577	67.4	131	2	A27472 Ig heavy chain precur	1.65e-68
16	577	67.4	139	2	PS0024 Ig heavy chain precur	1.65e-68
17	576	67.3	119	2	C30362 Ig heavy chain V regi	2.36e-68
18	576	67.3	139	1	MMH518 Ig heavy chain precur	2.36e-68
19	576	67.3	287	3	PC4402 haptan-specific singl	2.36e-68
20	575	67.2	142	2	A32483 Ig heavy chain V regi	3.38e-68
21	574	67.1	104	2	S69899 Ig heavy chain V regi	4.82e-68
22	574	67.1	117	2	JC2269 PL7-6 antibody heavy	4.82e-68
23	573	66.9	119	2	D30562 Ig heavy chain V regi	6.89e-68

24	573	66.9	120	2	S25175 Ig heavy chain V regi	6.89e-68
25	572	66.8	98	2	S26938 Ig heavy chain V regi	9.84e-68
26	572	66.8	116	2	S53751 antibody Fab Jel 103	9.84e-68
27	572	66.8	117	2	S18551 Ig heavy chain V regi	9.84e-68
28	572	66.8	117	2	G45722 anti-glycoprotein H m	9.84e-68
29	572	66.8	136	2	PL0208 Ig heavy chain precur	9.84e-68
30	571	66.7	116	2	PH0959 Ig heavy chain V regi	1.41e-67
31	571	66.7	118	1	KHMS38 Ig heavy chain V regi	1.41e-67
32	571	66.7	119	2	S45714 Ig heavy chain V regi	1.41e-67
33	571	66.7	119	2	E30562 Ig heavy chain V regi	1.41e-67
34	571	66.7	138	2	E32513 Ig heavy chain precur	1.41e-67
35	570	66.6	98	2	S26920 Ig heavy chain V regi	2.01e-67
36	570	66.6	135	2	PS0057 Ig heavy chain precur	2.01e-67
37	569	66.5	135	2	A30577 Ig heavy chain precur	2.87e-67
38	568	66.4	138	1	HVMS77 Ig heavy chain precur	4.10e-67
39	567	66.2	129	2	S46393 Ig heavy chain V regi	5.85e-67
40	567	66.2	137	1	G2MS43 Ig heavy chain precur	5.85e-67
41	566	66.1	117	1	HVHU35 Ig heavy chain precur	8.35e-67
42	566	66.1	137	2	S52445 Ig heavy chain V regi	8.35e-67
43	565	66.0	117	2	B27583 Ig heavy chain V regi	1.19e-66
44	565	66.0	117	1	HVHUHG Ig heavy chain precur	1.19e-66
45	565	66.0	117	2	S25176 Ig heavy chain V regi	1.19e-66

ALIGNMENTS

RESULT 1

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#accession

##status

##molecule_type

##residues

##cross-references

CLASSIFICATION

KEYWORDS

FEATURE

SUMMARY

Query Match

Best Local Similarity

Matches

Db

QY

Db

QY

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

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REFERENCE S48797
#authors Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
#submission submitted to the EMBL Data Library, October 1994
#description Molecular characterization of natural human anti-Sm
autoantibodies.
#accession S49530
#status preliminary
#molecule_type mRNA
#residues 1-135 #label MAH
#cross-references EMBL:Z46348; NID:g560839; PID:g560840
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE 34-117
SUMMARY #domain immunoglobulin homology #label IMM
#length 135 #molecular-weight 14997 #checksum 8132

Query Match 76.3%; Score 653; DB 2; Length 135;
Best Local Similarity 77.1%; Pred. No. 2.46e-80;
Matches 91; Conservative 10; Mismatches 15; Indels 2; Gaps 1;

Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFGYYMHVWRAPQGQGLEWGMWNPNSGGTNY 79
|||||
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFEYYMYWRAPQGQGLEWGMWNPNSGGTNY 60
|||||

Db 80 AOKFGQVTTTRDTISNTAYMELSLRSDDTAVYVCARGFY--NYWGQGLTVTVSS 135
|||||
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDDTAVYVCARGFNYRFAYWGQGLTVTVSS 118
|||||

RESULT 3
ENTRY D33548 #type complete
TITLE Ig heavy chain V-1 region (W1L2) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996

ACCESSIONS D33548
REFERENCE A33548
#authors Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
lymphocytic leukemia.
#cross-references MIMD:89345575
#accession D33548
#status preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
#molecule_type mRNA
#residues 1-123 #label KIP
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 123 #molecular-weight 13789 #checksum 9208

Query Match 71.6%; Score 613; DB 2; Length 123;
Best Local Similarity 73.2%; Pred. No. 4.25e-74;
Matches 90; Conservative 11; Mismatches 17; Indels 5; Gaps 2;

Db 1 QVQLVQSGAEVKKPGASVKVSCEASGYTFGYYMHVWRAPQGQGLEWGMWNPNSGGTNY 60
|||||
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFEYYMYWRAPQGQGLEWGMWNPNSGGTNY 60
|||||

Db 61 AOKFGQVTTTRDTISNTAYMELSLRSDDTAVYVCARGFYCGYDYFFDYWGQGLTVT 120
|||||
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDDTAVYVCARGF--N--YRFAYWGQGLTVT 115
|||||

Db 121 VSS 123
QY 116 VSS 118

RESULT 4
ENTRY S55542 #type fragment

TITLE Ig heavy chain V region pe2 - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
08-Sep-1997
ACCESSIONS S55542
REFERENCE S55528
#authors Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
#journal J. Mol. Biol. (1995) 247:932-946
#title Comprehensive epitope analysis of monoclonal
anti-proenkephalin antibodies using phage display libraries
and synthetic peptides: revelation of antibody fine
specificities caused by somatic mutations in the variable
region genes.
#accession S55542
#status preliminary
#molecule_type mRNA
#residues 1-116 #label BOE
#cross-references EMBL:X82581; NID:g854302; PID:g854303
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 14-97
SUMMARY #domain immunoglobulin homology #label IMM
#length 116 #checksum 418

Query Match 69.2%; Score 592; DB 2; Length 116;
Best Local Similarity 70.1%; Pred. No. 7.80e-71;
Matches 82; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

Db 1 VOLESGLAEVKKPGASVKLSCKASGYTFYYMYVWRQPGQGLEWIGFINSNGTNN 60
|||||
QY 2 VQLVQSGAEVKKPGASVKVSCKASGYTFEYYMYWRQPGQGLEWGRIDPEDGSIDY 61
|||||

Db 61 EKFKSKATLTVDKSSSTAYMOLSSLTSDSAVYCTRGWA--SMDYWGQGLTVTVSS 116
|||||
QY 62 EKFKKKVTLTADTSSSTAYMELSSLTSDTAVYVCARGFNYRFAYWGQGLTVTVSS 118
|||||

RESULT 5
ENTRY S20783 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
ACCESSIONS S20783
REFERENCE S20764
#authors Mortari, F.; Wang, J.; Schroeder, H.W.
#submission submitted to the EMBL Data Library, April 1992
#description Analysis of human cord blood Ig heavy chain IgA and IgG
repertoire.
#accession S20783
#status preliminary
#molecule_type DNA
#residues 1-121 #label MOR
#cross-references EMBL:Z11957; NID:g33899; PID:g33900
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 121 #molecular-weight 13033 #checksum 8006

Query Match 68.2%; Score 584; DB 2; Length 121;
Best Local Similarity 68.6%; Pred. No. 1.36e-69;
Matches 83; Conservative 13; Mismatches 22; Indels 3; Gaps 2;

Db 1 QVQLVQSGAEVKKPGASVTVSCASGYTFYFVHMVWRQAPQGQLEWGMNPHGSGTTF 60
|||||
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFEYYMYWRQAPQGQLEWGRIDPEDGSIDY 60
|||||

Db 61 AOKLQGRATVTRDTSTVYMDLSGRSEDTALYVCARGSDTSPASTIDYWGQGLTVTVS 120
|||||
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDTAVYVCARG--KF-NYRFAYWGQGLTVTVS 117
|||||

Db 121 S 121
QY 118 S 118
```

```

6
RESULT      S21810      #type complete
ENTRY       Ig heavy chain V region - mouse
TITLE       #formal_name Mus musculus #common_name house mouse
ORGANISM    20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
DATE        08-Sep-1997
ACCESSIONS  S21810
REFERENCE   Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
#authors    submitted to the EMBL Data Library, January 1991
#description Nucleotide sequence of a rearranged VDJ-region of a mouse Ig
            mu heavy chain gene and its upstream region.
#accession  S21810
#status     preliminary
#molecule_type DNA
#residues   1-138 #label OST
#cross-references EMBL:X56936; NID:g54163; RID:g54164.

GENETICS
#introns    15/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
34-117       #domain immunoglobulin homology #label IMM
SUMMARY       #length 138 #molecular-weight 15258 #checksum 1535
Query Match   68.1%; Score 583; DB 2; Length 138;
Best Local Similarity 68.9%; Pred. No. 1.94e-69;
Matches 82; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

Db 20 QVQLQSGPELVKPGASVTRISCKASGYTFYTHYHWKQPGGLEWIGWYGNVNTKY 79
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFYTHYHWKQPGGLEWIGWYGNVNTKY 60
Db 80 NEKFKGKATLTADKSSAYMQLSSLTSEDSAVYFCARGG-KFANDYWGQGTSTVTS 138
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYICARG-KFNRYFAYWGQGTSTVTS 118

7
RESULT      S38950      #type complete
ENTRY       Ig gamma chain - mouse
TITLE       #formal_name Mus musculus #common_name house mouse
ORGANISM    19-May-1994 #sequence_revision 10-Nov-1995 #text_change
DATE        23-May-1997
ACCESSIONS  S38950
REFERENCE   Kleibert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.;
#authors    Froesch, M.; Weisgerber, C.; Bitter-Suermann, D.;
            Hilschmann, N.
#journal     Biol. Chem. Hoppe-Seyler (1993) 374:993-1000
#title       Primary structure of the murine monoclonal IgG2a antibody
            mAb735 against alpha(2-8) polysialic acid. 2. Amino acid
            sequence of the heavy (H-) chain Fd' region.
#accession  S38950
#status     preliminary
#molecule_type protein
#residues   1-246 #label KLE
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS      immunoglobulin
FEATURE
137-201      #domain immunoglobulin homology #label IGG1
SUMMARY       #length 246 #molecular-weight 26216 #checksum 7059
Query Match   68.0%; Score 582; DB 2; Length 246;
Best Local Similarity 67.8%; Pred. No. 2.78e-69;
Matches 80; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Db 1 QIQLQSGPELVKPGASVKISCKASGYTFDYTHYHWKQPGGLEWIGWYGNVNTKY 60
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFYTHYHWKQPGGLEWIGWYGNVNTKY 60

#accession  S38950
#status     preliminary
#molecule_type protein
#residues   1-246 #label KLE
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS      immunoglobulin
FEATURE
137-201      #domain immunoglobulin homology #label IGG1
SUMMARY       #length 246 #molecular-weight 26216 #checksum 7059
Query Match   68.0%; Score 582; DB 2; Length 246;
Best Local Similarity 67.8%; Pred. No. 2.78e-69;
Matches 80; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Db 1 QIQLQSGPELVKPGASVKISCKASGYTFDYTHYHWKQPGGLEWIGWYGNVNTKY 60
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFYTHYHWKQPGGLEWIGWYGNVNTKY 60

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```

Db 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARGG-KFANDYWGQGTSTVTS 117
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYICARGKFNRYFAYWGQGTSTVTS 118

8
RESULT      S40295      #type complete
ENTRY       Ig gamma-2a chain (mAb735) - mouse
TITLE       #formal_name Mus musculus #common_name house mouse
ORGANISM    07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
DATE        23-May-1997
ACCESSIONS  S40295
REFERENCE   Kleibert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.;
#authors    Froesch, M.; Weisgerber, C.; Bitter-Suermann, D.;
            Hilschmann, N.
#submission submitted to the EMBL Data Library, January 1993
#description Primary structure of the murine monoclonal IgG2a antibody
            mAb735 against (2-8) polysialic acid. 2. Amino acid
            sequence of the heavy (H-) chain Fd' region.
#accession  S40295
#status     preliminary
#molecule_type protein
#residues   1-446 #label KLE
GENETICS
#map_position 12
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS      disulfide bond; glycoprotein; immunoglobulin; pyroglutamic
            acid
FEATURE
1-446        #product Ig gamma-2a chain #status experimental #label
            MAb
1-117        #domain V-D-J region #label VDJ
118-446      #domain C region #label CHR
118-214      #domain C1 region #label CH1
215-230      #region hinge
231-340      #domain C2 region #label CH2
341-446      #domain C3 region #label CH3
360-427      #domain immunoglobulin homology #label IGG3
1            #modified_site pyrrolidone carboxylic acid (Gln) #status
            experimental
22-96,144-199,
261-321,367-425
132          #disulfide_bonds #status predicted
132          #disulfide_bonds interchain (to light chain) #status
            predicted
224,227,229  #disulfide_bonds interchain #status predicted
297          #binding_site carbohydrate (Asn) (covalent) #status
            experimental
SUMMARY       #length 446 #molecular-weight 49108 #checksum 6356
Query Match   68.0%; Score 582; DB 2; Length 446;
Best Local Similarity 67.8%; Pred. No. 2.78e-69;
Matches 80; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Db 1 QIQLQSGPELVKPGASVKISCKASGYTFDYTHYHWKQPGGLEWIGWYGNVNTKY 60
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFYTHYHWKQPGGLEWIGWYGNVNTKY 60

9
RESULT      S25057      #type complete
ENTRY       Ig gamma-2b chain - mouse
TITLE       #formal_name Mus musculus #common_name house mouse
ORGANISM    19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
DATE        31-Oct-1997
ACCESSIONS  S25057
REFERENCE   Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch,
#authors      H.J.; Kreuzaler, F.
            submitted to the EMBL Data Library, July 1992
#submission

```

```
#description Production of a Tobacco mosaic virus (TMV) inactivating
#neotop specific monoclonal antibody in Nicotiana tabacum.
#accession S25057 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-474 #label FTS
#cross-references EMBL:456210; NID:954826; PID:954827
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY #length 474 #molecular-weight 52069 #checksum 4891

Query Match 68.0%; Score 582; DB 2; Length 474;
Best Local Similarity 67.2%; Pred. No. 2,78e-69;
Matches 80; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

Db 20 EVQLQSGPELVNPGASVKMSCKASGYTFITVYMHVWVKRQPGQGLEWIGYINPNKDKGTF 79
: ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTEYIMYWRQAPQGQLEMLGRIDPEDGSIDY 60
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 80 NEKEFGKATLTSKSSNTAYMELSLTSDSAVYYCARD-YDYDFWFGQGLTVTVSSA 137
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYYCARGKFN-YRFAYWGQGLTVTVSS 118
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 10
ENTRY PH1669 #type fragment
TITLE Ig heavy chain V region (clone 3B2) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change
16-Aug-1996
ACCESSION PH1669
REFERENCE PH1642
#authors Hillison, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso,
E.H.
#journal J. Exp. Med. (1993) 178:331-336
#title The structural basis of germline-encoded VH3 immunoglobulin
binding to staphylococcal protein A.
#accession PH1669
#molecule_type mRNA
#residues 1-110 #label H1L
#experimental_source B cell
#classification #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
FEATURE 7-90
SUMMARY #domain immunoglobulin homology #label IMM
#length 110 #checksum 8449

Query Match 67.9%; Score 581; DB 2; Length 110;
Best Local Similarity 72.7%; Pred. No. 3,97e-69;
Matches 80; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Db 1 AEVKKPGASVKSCASGYTFITGYIMHWVRQAPGQGLEWMGRINANSQGTNYAQRFGQRV 60
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 9 AEVKKPGASVKSCASGYTFTEYIMYWRQAPGQGLEMLGRIDPEDGSIDYVEKFKKV 68
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

Db 61 TMTDRTSITAYMELSLRSDTAVYYCARDLTGDAFDWGQGLTVTVSS 110
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 69 TLTADTSSSTAYMELSLTSDTAVYYCARGKFNRYFAYWGQGLTVTVSS 118
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 11
ENTRY C30560 #type fragment
TITLE Ig heavy chain V region (35.8.2H) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change
20-Mar-1998
ACCESSION C30560
REFERENCE A30560
#authors Matsuda, T.; Kabat, E.A.
#journal J. Immunol. (1989) 142:863-870
#title Variable region cDNA sequences and antigen binding
specificity of mouse monoclonal antibodies to isomaltosyl
oligosaccharides coupled to proteins. T-dependent analogues
of alpha(1->6)dextran.
```

```
#cross-references MUID:89110062
#accession C30560 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-118 #label MAT
#cross-references GB:M24270; NID:9195615; PID:9195616
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 118 #checksum 9448

Query Match 67.9%; Score 581; DB 2; Length 118;
Best Local Similarity 68.9%; Pred. No. 3,97e-69;
Matches 82; Conservative 16; Mismatches 19; Indels 2; Gaps 2;

Db 1 QVHLQSGAEVKKPGASVKISCKASGYTFITSYMMWVRQAPGQGLEWIGEDIPSNSTYN 60
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTEYIMYWRQAPQGQLEMLGRIDPEDGSIDY 60
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 61 NQKFNKATLTVKSSNTAYMQLSLTSDSAVYYCARWGT-GSWFAYWGQGLTVTVSSA 118
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYYCAR-GKFNRYFAYWGQGLTVTVSS 118
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 12
ENTRY S31600 #type fragment
TITLE Ig heavy chain V region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
ACCESSION S31600
REFERENCE S31585
#authors Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
Tonnel, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in fetal liver.
#accession S31600
#status preliminary
#molecule_type mRNA
#residues 1-136 #label CUI
#cross-references EMBL:214165; NID:930994; PID:930995
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
FEATURE 34-117
SUMMARY #domain immunoglobulin homology #label IMM
#length 136 #checksum 9862

Query Match 67.8%; Score 580; DB 2; Length 136;
Best Local Similarity 70.3%; Pred. No. 5,67e-69;
Matches 83; Conservative 15; Mismatches 18; Indels 2; Gaps 2;

Db 20 QVQLVQSGAEVKKPGASVKVCKASGYTFITVDINVRQATQGGLEWMGNPNSTGY 79
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTEYIMYWRQAPQGQLEMLGRIDPEDGSIDY 60
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 80 AQKQGRVTMTNYSISTAYMELSLRSDTAVYYCARWR-D-AFDWGQGLTVTVSS 135
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYYCARGKFNRYFAYWGQGLTVTVSS 118
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 13
ENTRY PH0962 #type fragment
TITLE Ig heavy chain V region (G6+ T-L42) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSION PH0962
REFERENCE PH0952
#authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
```

```

#cross-references MUID:92202880
#accession PH0962
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-120 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30
15-98 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-108 #region complementarity-determining 3
SUMMARY
#length 120 #checksum 5559
Query Match 67.4%; Score 579; DB 2; Length 120;
Best Local Similarity 73.3%; Pred. No. 8.10e-69;
Matches 88; Conservative 10; Mismatches 20; Indels 2; Gaps 1;
Db 1 QVQLVQSGAEVKKPGASVKSCASGFTFSYAIISWRQAPGGQGLEWMGGIPIFGTANY 60
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFTEYYMYWRQAPGGQGLEMLGRIDPDGSIDY 60
Db 61 AKFGQGRVITADESTAYMELSLRSEDTAVYYCARGGVAGRPHPFDYWGQGLTVTVSS 120
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDTAVYYCARGKFNRY--FAYWGQGLTVTVSS 118

RESULT 14
ENTRY B22769 #type complete
TITLE Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
16-Aug-1996
ACCESSION B22769
REFERENCE A90971
#authors Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.;
Beyreuther, K.
#journal EMBO J. (1982) 1:635-640
#title Immunoglobulin V region variants in hybridoma cells. II.
#cross-references MUID:84236026
#accession B22769
#molecule_type protein
#residues 1-120 #label DIL
#note the sequences of two spontaneously arising somatic
variants, B1-8.V1 and B1-8.V2, appear to be identical;
the differ from the B1-8 at 10 positions, most of
which occur in the CDR2 region
#note peptides and unsequenced residues were positioned by
homology with the B1-8 sequence
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY
#length 120 #molecular_weight 13465 #checksum 432
Query Match 67.4%; Score 577; DB 2; Length 120;
Best Local Similarity 68.3%; Pred. No. 1.65e-68;
Matches 82; Conservative 13; Mismatches 23; Indels 2; Gaps 2;
Db 1 QVQLQPGAEIVKPGASVKSCASGYTFTSYMMHWKQRPQGGLDWIGEINPSNGRTNY 60
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFTEYYMYWRQAPGGQGLEMLGRIDPDGSIDY 60
Db 61 NQKFKKATLTVDKPSSTAYMOLSSLTSEDSAVYCYDYSSYFYDYGQGLTVTVSS 120
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDTAVYYCAR-GKFNRY--FAYWGQGLTVTVSS 118

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```

RESULT 15
ENTRY A27472 #type fragment.
TITLE Ig heavy chain precursor V region (IE9) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
18-Oct-1996
ACCESSION A27472
REFERENCE A27472
#authors Liu, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
#journal Gene (1987) 54:33-40
#title Expression of mouse::human immunoglobulin heavy-chain cDNA in
lymphoid cells
#cross-references MUID:87277430
#accession A27472
#molecule_type mRNA
#residues 1-131 #label LIU
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
5-54 #region complementarity-determining 1\
20-131 #product Ig heavy chain V region IE9 #status predicted
#label MAT\
34-117 #domain immunoglobulin homology #label IMM\
69-85 #region complementarity-determining 2\
118-125 #region complementarity-determining 3\
SUMMARY
#length 131 #checksum 1501
Query Match 67.4%; Score 577; DB 2; Length 131;
Best Local Similarity 69.3%; Pred. No. 1.65e-68;
Matches 79; Conservative 16; Mismatches 16; Indels 3; Gaps 3;
Db 20 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYMMHWKQRPQGGLDWIGEINPSNGRTNY 79
QY 1 QVQLVQSGAEVKKPGASVKYSCASGYTFTEYYMYWRQAPGGQGLEMLGRIDPDGSIDY 60
Db 80 NEKFKKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA-S-YDYDFAYWGQGLT 131
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDTAVYYCARGKFNRY--FAYWGQGLT 113

```

Search completed: Thu Jan 14 17:14:47 1999
Job time : 17 secs.

M P S R E L I

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:13:15 1999; MasPar time 5.76 Seconds

Tabular output not generated. 549,423 Million cell updates/sec

Title: >US-08-477-989B-93
Description: (1-118) from US08477989B.pep
Perfect Score: 856
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....GKFNRYFAYWGQGLTLTVSS 118

Scoring table: PAM 150
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swissprot

Statistics: Mean 42.127; Variance 73.640; scale 0.572

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	576	67.3	139	1	HV07_MOUSE IG HEAVY CHAIN PRECURS	2.56e-103
2	571	66.7	118	1	HV51_MOUSE IG HEAVY CHAIN V REGIO	3.66e-102
3	569	66.5	117	1	HV13_MOUSE IG HEAVY CHAIN V REGIO	1.06e-101
4	568	66.4	138	1	HV48_MOUSE IG HEAVY CHAIN PRECURS	1.81e-101
5	567	66.2	137	1	HV11_MOUSE IG HEAVY CHAIN PRECURS	3.07e-101
6	566	66.1	117	1	HV1G_HUMAN IG HEAVY CHAIN PRECURS	5.23e-101
7	565	66.0	117	1	HV1B_HUMAN IG HEAVY CHAIN PRECURS	8.89e-101
8	556	65.0	117	1	HV12_MOUSE IG HEAVY CHAIN V REGIO	1.06e-98
9	541	63.2	120	1	HV50_MOUSE IG HEAVY CHAIN V REGIO	3.00e-95
10	539	63.0	140	1	HV02_MOUSE IG HEAVY CHAIN PRECURS	8.66e-95
11	521	60.9	117	1	HV09_MOUSE IG HEAVY CHAIN PRECURS	1.18e-90
12	520	60.7	120	1	HV03_MOUSE IG HEAVY CHAIN V REGIO	1.99e-90
13	513	59.9	117	1	HV04_MOUSE IG HEAVY CHAIN PRECURS	8.00e-89
14	511	59.7	117	1	HV06_MOUSE IG HEAVY CHAIN PRECURS	2.30e-88
15	505	59.0	117	1	HV10_MOUSE IG HEAVY CHAIN PRECURS	5.41e-87
16	503	58.8	114	1	HV00_MOUSE IG HEAVY CHAIN V REGIO	1.55e-86
17	503	58.8	143	1	HV1C_HUMAN IG HEAVY CHAIN PRECURS	1.55e-86
18	500	58.4	117	1	HV49_MOUSE IG HEAVY CHAIN PRECURS	7.52e-86
19	490	57.2	136	1	HV15_MOUSE IG HEAVY CHAIN PRECURS	1.44e-83
20	489	57.1	117	1	HV05_MOUSE IG HEAVY CHAIN PRECURS	2.44e-83
21	487	56.9	117	1	HV52_MOUSE IG HEAVY CHAIN PRECURS	6.96e-83
22	484	56.5	117	1	HV14_MOUSE IG HEAVY CHAIN PRECURS	3.36e-82
23	480	56.1	121	1	HV01_MOUSE IG HEAVY CHAIN V REGIO	2.74e-81

24	476	55.6	120	1	HV1H_HUMAN IG HEAVY CHAIN V-I REG	2.22e-80
25	465	54.3	117	1	HV1A_HUMAN IG HEAVY CHAIN V-I REG	7.04e-78
26	459	53.6	119	1	HV40_MOUSE IG HEAVY CHAIN V REGIO	1.61e-76
27	457	53.4	119	1	HV37_MOUSE IG HEAVY CHAIN V REGIO	4.58e-76
28	455	53.2	122	1	HV3G_HUMAN IG HEAVY CHAIN V-III R	1.30e-75
29	435	50.8	119	1	HV38_MOUSE IG HEAVY CHAIN V REGIO	4.30e-71
30	435	50.8	122	1	HV3A_HUMAN IG HEAVY CHAIN V-III R	4.30e-71
31	434	50.7	117	1	HV42_MOUSE IG HEAVY CHAIN V REGIO	7.23e-71
32	425	49.6	117	1	HV03_CARAU IG HEAVY CHAIN PRECURS	7.69e-69
33	422	49.3	117	1	HV17_MOUSE IG HEAVY CHAIN V REGIO	3.63e-68
34	422	49.3	121	1	HV3J_HUMAN IG HEAVY CHAIN V-III R	3.63e-68
35	421	49.2	124	1	HV1D_HUMAN IG HEAVY CHAIN V-I REG	6.10e-68
36	421	49.2	125	1	HV1F_HUMAN IG HEAVY CHAIN V-I REG	6.10e-68
37	420	49.1	136	1	HV16_MOUSE IG HEAVY CHAIN PRECURS	1.02e-67
38	419	48.9	142	1	HV01_RAT IG HEAVY CHAIN PRECURS	1.72e-67
39	416	48.6	117	1	HV41_MOUSE IG HEAVY CHAIN V REGIO	8.09e-67
40	415	48.5	119	1	HV31_HUMAN IG HEAVY CHAIN V-III R	1.36e-66
41	414	48.4	116	1	HV3T_HUMAN IG HEAVY CHAIN V-III R	2.27e-66
42	413	48.2	124	1	HV1E_HUMAN IG HEAVY CHAIN V-I REG	3.81e-66
43	412	48.1	115	1	HV3D_HUMAN IG HEAVY CHAIN V-III R	6.39e-66
44	411	48.0	118	1	HV39_MOUSE IG HEAVY CHAIN V REGIO	1.07e-65
45	399	46.6	120	1	HV3U_HUMAN IG HEAVY CHAIN V-III R	5.19e-63

ALIGNMENTS

RESULT 1
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA BOWENELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTIBODIES)
DR EMBL; J00529; G195115;
DR PIR; A02034; MHWS18.
DR HSP; P01810; IJHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION (B1-8 / 186-2).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; DEB2C7DA CRC32;

Query Match 67.3%; Score 576; DB 1; Length 139;
Best Local Similarity 68.3%; Pred. No. 2.56e-103;
Matches 82; Conservative 14; Mismatches 22; Indels 2; Gaps 2;

Db 20 QVQLVQSGAEVKKPGASVKLSCKASGYTFTSYMMHWKQRCRGLEWIGRIDPNSGKTKY 79
Oy 1 QVQLVQSGAEVKKPGASVKSKASGYTFTSYMMHWKQRCRGLEWIGRIDPNSGKTKY 60
Db 80 NEKFKSKATLVDKPPSSPAYMQLSLTSEDGAVVYCARVDYVGSFYDWGQGLTLTVSS 139

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QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFTFTFYWMYWRQAPGQGLMGRIDPDGSDY 6
Db 61 NOKEFGKATLTVDKSSSTAYMQLNSLTSEDSAVYICSCARDRYW-FDVMGAGTTVTVSS 117
QY 61 VEKEFKKVTLTADTSSSTAYMELSSLTSDTAVYICARGFNFRFAVWGQGLTVTVSS 118

RESULT 4
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (REL. 02, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 84248078.
RX KILLAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,
RA TUCKER P.W.
RL PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR HSP; P01810; IJHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION (TEPC 1017).
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; BEF6247B CRC32;

Query Match 66.4%; Score 568; DB 1; Length 138;
Best Local Similarity 66.4%; Pred. No. 1.81e-201;
Matches 79; Conservative 18; Mismatches 21; Indels 1; Gaps

Db 20 QVQLQPGAEVLKPGASVQLSCKASGHTFTFYWMYWRQAPGQGLEWGEINPDGRSNY 79
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFTFTFYWMYWRQAPGQGLMGRIDPDGSDY 61
Db 80 NEKFNKATLTVDKSSSTAYMQLSSLTPEEFAYVYICARSDGYDFWYWGQGLTVTVSS 138
QY 61 VEKEFKKVTLTADTSSSTAYMELSSLTSDTAVYICARGFNFRFAVWGQGLTVTVSS 118

RESULT 5
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (S43).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 81234548.
RX BATHWELL A.L.M., PASKING M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTMORE D.;
RL CELL 24:625-637(1981).
CC -1- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTIBODIES).
DR EMBL; J00539; G195119;
DR PIR; A02038; G2M543.

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DR HSP: P01772; LFV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION (S43).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; C37539BD CRC32;

Query Match 66.2%; Score 567; DB 1; Length 137;
Best Local Similarity 68.1%; Pred. No. 3.07e-101;
Matches 81; Conservative 14; Mismatches 22; Indels 2; Gaps 2;

Db 20 QVQLVQSGAEVFKPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 79
QY 1 QVQLVQSGAEVFKPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 79
Db 80 NEHFRSKATLTIDKPSSTAYMQLSLTSDSAVYICARYLGRY-FDYWGQGTLLTVSS 137
QY 61 VERFKKVTLTADTSSSTAYMELSSLTSDTAVYICARGKEN-YRFAYWGQGTLLTVSS 118

RESULT 6
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (V35).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
RA OHNO H., FUKUHARA S., HONJO T.;
RL EMBO J. 7:1047-1051(1988).
DR EMBL; X07448; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSP; P01810; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; FAA560D1 CRC32;

Query Match 66.1%; Score 566; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 5.23e-101;
Matches 78; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Db 20 QVQLVQSGAEVFKPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 79
QY 1 QVQLVQSGAEVFKPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 79
Db 80 AQKFGQVTRTSTSTAYMELSSLTSDTAVYICAR 117
QY 61 VERFKKVTLTADTSSSTAYMELSSLTSDTAVYICAR 98

RESULT 7
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (HG3).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88296408.
RA MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
RA OHNO H., FUKUHARA S., HONJO T.;
RL EMBO J. 7:1047-1051(1988).
DR EMBL; X07448; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSP; P01810; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; FAA560D1 CRC32;

Query Match 66.1%; Score 566; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 5.23e-101;
Matches 78; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Db 20 QVQLVQSGAEVFKPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 79
QY 1 QVQLVQSGAEVFKPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 79
Db 80 AQKFGQVTRTSTSTAYMELSSLTSDTAVYICAR 117
QY 61 VERFKKVTLTADTSSSTAYMELSSLTSDTAVYICAR 98

RESULT 8
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 83075344.
RA KERRY M.R., FUHRMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
RA HOOD L.E.;
RL BIOCHEMISTRY 21:5415-5424(1982).
CC -|- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS
CC -|- ALSO BEEN DETERMINED.
CC -|- THIS PROTEIN BINDS DEXTRAN.
DR HSP; P01772; LFV.
DR PIR; A02039; MHMS4E.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 1F6CC304 CRC32;

Query Match 65.0%; Score 556; DB 1; Length 117;
Best Local Similarity 64.4%; Pred. No. 1.06e-98;
Matches 76; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

Db 1 EVOLQSQSPGLVPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 60
QY 1 EVOLQSQSPGLVPGASVKSLCKASGYTFYSLMHVNWNPQPGGLEWGRIDPNSGGTTY 60
Db 61 NOKEFKATLTVDKSSSTAYMQLSLTSDSAVYICARD-YDYFVDMGAGTTLTVSS 117
QY 61 VERFKKVTLTADTSSSTAYMELSSLTSDTAVYICARGKEN-YRFAYWGQGTLLTVSS 118

RESULT 9
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;

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Db      140 S 140
QY      118 S 118

RESULT 11
ID HV03_MOUSE STANDARD; PRT; 117 AA.
AC PO1753; P11271;
DT 21-JUL-1986 (REL. 01, CREATED)
DT DT 21-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (186-1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE; 81234548.
RA BOWTHELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RL BALTIMORE D.;
RA CELL 24:625-637(1981).
CC -! THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR; B02034; HVM561.
CC HSSP; P01810; 1FVB.
CR IMMUNOGLOBULIN V REGION; SIGNAL.
DR SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (186-1).
FT DOMAIN 20 49 FRAMEWORK 1.
FT .DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFD 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12890 MW; C97683A2 CRC32;

Query Match 60.9%; Score 521; DB 1; Length 117;
Best Local Similarity 73.5%; Pred.No.1.18e-90;
Matches 72; Conservative 11; Mismatches 15; Indels 0; Gaps 0

Db      20 QVLOQPQGAELVKPGASVKLSCKASGYTFSTYMMHWKQPRGLEGWIGRIDPNSGGTKY 79
QY      1 QVLVSQAEVKPGASVKYSCKASGYTFEYYMYWVRQAPGGQLMGLGRDPEDGSIDI 60
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db      80 NEKFASKATLVDSSTSTAYMWLHSLTSDSAVIYICAR 117
QY      61 VEKFKKKVTLTADTSSTSTAYMELSSLTSDTTAVYICAR 98
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC PO1747;
DT 21-JUL-1986 (REL. 01, CREATED)
DT DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (36-65).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 83131846.
RX SIEKEVITZ M., GEFTER M.L., BRODEUR P., RIBLET R.,
RA MARSHAK-ROTHSTEIN A.;
RL EUR. J. IMMUNOL. 12:1023-1032(1982).
CC -! FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
CC THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
CC THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
CC PIR; A02028; HVM5G7.
CC HSSP; P01789; 16FAB.
CR IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA.

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RP  SEQUENCE FROM N.A.
RC  STRAIN-C57BL/6;
RX  MEDLINE; 81234548.
RA  BOWTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA  BALTIMORE D.;
RL  CELL 24:625-637(1981).
CC  -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC  THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR  PIR: A02032; HYMS02.
DR  HSP: P01810; 1JHL.
KW  IMMUNOGLOBULIN V REGION; SIGNAL.
FT  SIGNAL 1 19
FT  CHAIN 20 117
FT  DOMAIN 20 49
FT  DOMAIN 50 54
FT  DOMAIN 55 68
FT  DOMAIN 69 85
FT  DOMAIN 86 117
FT  DISULFID 41 115
FT  NON_TER 117 117
SQ  SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;

Query Match 59.7%; Score 511; DB 1; Length 117;
Best Local Similarity 72.2%; Pred.No. 2.30e-88;
Matches 70; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Db 20 HVQLQOPGAELVPGASVKSCASGVFTSYVMHWVKRPGGLEWIGRIHPDSDDTVY 79
Qy 1 QVQLVQSGAEVKKPGASVKSCASGVFTFEYIMYWRAPGGLEUMGRIDPEDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKEKGRATITVQKSSSTAYMQLSSLTSEDSAVYYCA 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 VEKEFKKVTLTADTSSTAYMELSSLTSDTAVYYCA 97
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (145).
DE MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA BOWTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR ENBL; J00533; G554033;
DR PIR: C02034; HYMS45.
DR HSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D9E6B000 CRC32;

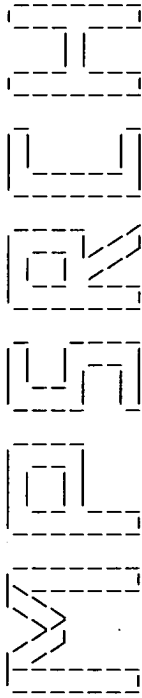
Query Match 59.08; Score 505; DB 1; Length 117;
Best Local Similarity 71.4%; Pred.No. 5.41e-87;
Matches 70; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Db 20 QVQLVQSGAEVKKPGASVKSSKASGVFTSYVMHWVKRPGGLEWIGRIHPDSDDTVY 79

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QY 1 QVQLVQSGAEVKPGASVKYSCKASGYTFEYYMWVVRQAPGQGLELMGRIDPDGSDY 60
Db 80 NEKFKSKATLTVDKPSSTAYNQLSSLTSEDSAVYYCAR 117
QY 61 VEFKKKVTLTADTSSSTAYMELSSLTSDDTAVYYCAR 98

Search completed: Thu Jan 14 17:13:28 1999
Job time : 13 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:13:47 1999; MasPar time 11.40 Seconds
Tabular output not generated. 515.642 Million cell updates/sec

Title: >US-08-477-989B-93
Description: (1-118) from US08477989B.pap
Perfect Score: 856
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....GKFNRYFAYWGQGLTVTVSS 118

Scoring table: PAM 150
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sprembl6
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 40.641; Variance 74.227; scale 0.548

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description	ID	Pred. No.
1	629	73.5	PLATELET MEMBRANE GLYC	Q99846	3.55e-111
2	617	72.1	IGM HEAVY CHAIN (FRAGM	009199	1.59e-108
3	590	68.9	SINGLE-CHAIN FV FRAGME	000288	1.72e-102
4	575	67.2	IGG HEAVY CHAIN (FRAGM	009200	3.67e-99
5	569	66.5	RHEUMATOID FACTOR RF-E	043222	7.86e-98
6	553	64.6	OKT3 HEAVY CHAIN VARIA	P70173	2.74e-94
7	546	63.8	ANTI-CD30 MOAB KI-4 SC	035140	9.66e-93
8	545	63.7	TYPE II COLLAGEN ANTIB	P37407	1.61e-92
9	531	62.0	ANTIGEN, B-CELL RECEPT	Q61250	1.98e-89
10	526	61.4	ANTI-DNA HEAVY CHAIN (061218	2.50e-88
11	526	61.4	SINGLE CHAIN FV ANTIBO	P97512	2.50e-88
12	516	60.3	MONOCLONAL ANTIBODY ID	P97746	3.97e-86
13	512	59.8	ANTI-ACID PHOSPHATASE	035529	3.01e-85
14	507	59.2	ANTI-CEA 79 SINGLE CHA	P37771	3.78e-84
15	504	58.9	A6 ANTI-[4-HYDROXY-3-N	055113	1.72e-83
16	503	58.8	RHEUMATOID FACTOR RF-I	043220	2.86e-83
17	503	58.8	CC49 FAB PRECURSOR (FR	Q61552	2.86e-83
18	501	58.5	ANTI-ACID PHOSPHATASE	035528	7.85e-83
19	489	57.1	ANTI-HIV-1 GP120 V3 LO	Q99825	3.35e-80
20	483	56.4	RHEUMATOID FACTOR RF-E	043221	6.89e-79

21	470	54.9	129	4	Q99823	ANTI-HIV-1 GP120 ANTIB	4.77e-76
22	468	54.7	124	4	Q99824	ANTI-HIV-1 GP120 ANTIB	1.30e-73
23	440	51.4	125	11	054733	MA-15 HEAVY CHAIN (FRA	1.61e-69
24	439	51.3	100	4	043235	RHEUMATOID FACTOR RF-I	2.65e-69
25	426	49.8	136	4	Q99821	ANTI-HIV-1 GP120 ANTIB	1.73e-66
26	416	48.6	120	4	092477	ANTI-FOLATE BINDING PR	2.50e-66
27	413	48.2	248	11	063818	IMMUNOTOXIN MIK-BETA 1	1.11e-63
28	412	48.1	239	4	043690	ANTI-MPL SCFV (FRAGMEN	1.82e-63
29	412	48.1	240	4	000289	SINGLE-CHAIN FV FRAGME	1.82e-63
30	400	46.7	119	4	Q15987	RHEUMATOID FACTOR D5 H	6.96e-61
31	398	46.5	244	4	043689	ANTI-HER3 SCFV (FRAGME	1.87e-60
32	392	45.8	122	4	Q99817	ANTI-SSDNA ANTIBODY HE	3.62e-59
33	383	44.7	137	4	095670	MONOCLONAL ANTIBODY HE	3.08e-57
34	383	44.7	147	4	Q13667	VH3-IG HEAVY CHAIN VAR	3.08e-57
35	379	44.3	98	4	043226	RHEUMATOID FACTOR RF-I	2.19e-56
36	369	43.1	119	4	Q15983	RHEUMATOID FACTOR C6 H	2.97e-54
37	367	42.9	117	11	Q61195	ANTI-CARCINOMA EMBRYON	7.92e-54
38	358	41.8	122	4	095050	HEAVY CHAIN FAB FRAGME	6.47e-52
39	357	41.7	98	4	043228	RHEUMATOID FACTOR RF-I	1.05e-51
40	355	41.5	96	4	043224	RHEUMATOID FACTOR RF-I	2.80e-51
41	347	40.5	115	4	043230	RHEUMATOID FACTOR RF-E	1.38e-49
42	345	40.3	121	11	070568	SINGLE CHAIN FV (FRAGM	3.66e-49
43	338	39.5	121	4	015526	HRV FAB 026-VH (FRAGME	1.09e-47
44	337	39.4	96	4	043227	RHEUMATOID FACTOR RF-I	1.78e-47
45	337	39.4	116	4	Q99515	HEAVY CHAIN FAB FRAGME	1.78e-47

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	125 AA.
ID	Q99846			
AC	Q99846;			
DT	01-MAY-1997 (TREMBLREL. 03, CREATED)			
DT	01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	PLATELET MEMBRANE GLYCOPROTEIN IB (GP1B) SPECIFIC ANTIBODY (FRAGMENT).			
GN	VI-02.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 91370594.			
RA	HIRAIWA A., NUGENT D.J., MILNER E.C.;			
RL	AUTOIMMUNITY 8:107-113(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	GLAS A.M., MILNER E.C.B.;			
RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; U86522; GI816664;			
DR	PFAM; PF00047; Ig.			
FT	NON_TER 1 1			
FT	NON_TER 125 125			
SO	SEQUENCE 125 AA; 13722 MW; 8576EE5A CRC32;			
Query Match 73.5%; Score 629; DB 4; Length 125;				
Best Local Similarity 73.6%; Pred. No. 3.55e-111;				
Matches 89; Conservative 11; Mismatches 18; Indels 3; Gaps 2;				
Db	1	QVQLVQSGAEVKKPGASVKASGYFTFTDYIMHWVRQAPQGLEWMGRINPNSGGTKY 60		
Qy	1	QVQLVQSGAEVKKPGASVKASGYFTFTDYIMHWVRQAPQGLEWMGRIDPEDGSIDY 60		
Db	61	AEKFGQRTMTDTSISAVYHLSRLSRDSDTAVYVCARVLRVGCATFAFIWQGGTWTVS 120		
Qy	61	VEKFKKVTLTADTSSSTAYMELSLTSDTAVYVCARG-KFNRYFAY--WGQGLTVTVS 117		
Db	121	S 121		
Qy	118	S 118		
RESULT	2			

[illegible]

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RP SEQUENCE FROM N.A.
RX MEDLINE; 97058313.
RA ARAKAWA F., KUROKI M., KUWAHARA M., SENBA T., OZAKI H., MATSUOKA Y.,
RA MISUMI Y., KANDA H., WATANABE T.;
RL J. BIOCHEM. 120:657-662(1996).
DR EMBL; D82081; G1565186;
DR PFAM; PF00047; ig.
KW SIGNAL.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 >138 ORT3 HEAVY CHAIN VARIABLE REGION.
FT NON_TER 138
SQ SEQUENCE 138 AA; 15648 MW; 75D6DD0A CRC32;

Query Match 64.68; Score 553; DB 11; Length 138;
Best Local Similarity 68.18; Pred. No. 2.74e-94;
Matches 81; Conservative 15; Mismatches 22; Indels 1; Gaps 1;

Db 20 QVQLQSGAELAPGASVKSCASGYTFRTYTHHWKORPGQGLEWIGYINPGRYNY 79
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKKATLTDDKSSSTAYMQLSLSEDSAVYICARYDDHYCLDYWGQGLTIVSS 138
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VERFKKVTLTADTSSTAYMQLSLSEDSAVYICARYDDHYCLDYWGQGLTIVSS 118
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
ID Q35140 PRELIMINARY; PRT; 243 AA.
AC Q35140;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ANTI-CD30 MOAB KI-4 SCFV (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA KLIMKA A., BARTH S., MATTHEY B., LEMKE H., ARENDS J.W., DIEHL V.,
RA HOOGENDOORN H., ENGERT A.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF002242; G2290774;
DR PFAM; PF00047; ig.
FT NON_TER 1 1
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 26225 MW; E0AD5383 CRC32;

Query Match 63.88; Score 546; DB 11; Length 243;
Best Local Similarity 64.28; Pred. No. 9.66e-93;
Matches 77; Conservative 19; Mismatches 22; Indels 2; Gaps 2;

Db 1 QVQLQSGTELAKPGAAVKSCASGYTFRTYTHHWKORPGQGLEWIGYINPNTAYTDY 60
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKKATLTADKSSSTAYMQLSLSEDSAVYICARYDDHYCLDYWGQGLTIVSS 120
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
ID P97407 PRELIMINARY; PRT; 111 AA.
AC P97407;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE TYPE II COLLAGEN ANTIBODY HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/1J;

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RX MEDLINE; 97257994.
RA ITO-H.O., UEDA T., HASHIMOTO Y., IMOTO T., KOGA T.;
RA CELL. MOL. LIFE SCI. 53:51-60(1997).
DR EMBL; U69538; G1731665;
DR PFAM; PF00047; ig.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12444 MW; 6A22312F CRC32;

Query Match 63.7%; Score 545; DB 11; Length 111;
Best Local Similarity 65.8%; Pred. No. 1.61e-92;
Matches 73; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

Db 1 QVQLQSGAELAKPGTSVKMSCKASGYTLISYIMNWKORPGQGLEWIGAINPSNYTEY 60
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKKATLTADKSSSTAYMQLSLSEDSAVYICAREDYGSTHFDYWGQ 111
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
ID Q61250 PRELIMINARY; PRT; 152 AA.
AC Q61250;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTIGEN, B-CELL RECEPTOR PRECURSOR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE; 96134009.
RA THIRION S., MOTMANS K., HEYLIGEN H., RAUS J., VANDEVYVER C.;
RL IMMUNOGENETICS 43:167-168(1996).
DR EMBL; L43567; G899071;
DR PFAM; PF00047; ig.
KW SIGNAL.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 152 ANTIGEN, B-CELL RECEPTOR.
SQ SEQUENCE 152 AA; 16517 MW; A83E9253 CRC32;

Query Match 62.0%; Score 531; DB 11; Length 152;
Best Local Similarity 65.0%; Pred. No. 1.98e-89;
Matches 78; Conservative 17; Mismatches 23; Indels 2; Gaps 2;

Db 20 QVQLQSGPELVKPGASVKMSCKASGYKFSVSHWVKQKAGQGLEWIGYINPNDVTKY 79
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKKATLTADKSSSTAYMQLSLSEDSAVYICARSAYDYDGIAYWGQGLTIVSS 139
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFEYIMYWRQAPQGQLEMLGRIDPDGSIDY 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
ID Q61218 PRELIMINARY; PRT; 123 AA.
AC Q61218;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ANTI-DNA HEAVY CHAIN (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C3H/HEJ-LPR/LPR;
RA WLOCH M.K., ALEXANDER A.L., PIPPEN A.M.M., PISETSKY D.S.,

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OC EUTHERIA; RODENTIA.
RN [1] .....
RP SEQUENCE FROM N.A.
RX MEDLINE; 96366461.
RA KIMURA N., YOSHIKAWA H., IWAMOTO M., SAKIHAMA T., AKASU F., IZUI S.,
RA UENO A., NAKAJIMA Y., TASAKA K.;
RL HYBRIDOMA 14:523-528(1995).
RR DR EMBL; S82857; G1835936; -.
DR PFAM; PF00047; ig.
FT NON_TER 1
SQ SEQUENCE 120 AA; 13147 MW; 3EA54DB8 CRC32;

Query Match 60.3%; Score 516; DB 11; Length 120;
Best Local Similarity 62.5%; Pred. No. 3.97e-86;
Matches 75; Conservative 17; Mismatches 25; Indels 3; Gaps

Db 1 VOLQSQGTVLARPCGKASVKMCKASGYTFTSYVMHWHVQRPGQGLEWICAIYPGNSDTSYN 60
||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| : : : |||
QY 2 VOLVQSGAEVKKPCASVKVCKASGYITFTYYMVTWVQAPQGLELMGRIDPEDGSIDYV 61
||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| : : : |||

Db 61 QKFKGKAKLTAFTVTSASTAYMELSSLTNEDSGAVYCTRDYDYGSSGAFDYWGQGTTLTVSS 12
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OV 62 EKFKKVTTLADTSSSPAYMELSSLTSDDTAVVYCAKGEN-YR--PAYMGCGTLTVTVSS 11
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT	13
ID	Q35529 PRELIMINARY; PRPT; 116 AA.
AC	Q35529;
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE	ANTI-ACID PHOSPHATASE VARIABLE HEAVY CHAIN 18 (FRAGMENT).
CS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/C;
RA	TAKAYA R., MIYAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MIYAMOTO T.
RA	HATANO S.;
RL	SUBMITTED (APR-1995) TO EMBL/GENEBANK/DDBJ DATA BANKS.
DR	EMBL; D50137; D1024480; -.
DR	PFAM; PF00047; 1g.
FT	NON_TER 1
FT	NON_TER 116 116
FT	SEQUENCE 116 AA; 13097 MW; BEFF6E1A CRC32;
SQL	
Query Match	59.8%; Score 512; DB 11; Length 116;
Best Local Similarity	61.0%; Pred. No. 3.01e-85;
Watches	72; Conservative
	19; Mismatches 25; Idels 2.

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Db      1  QLKQESGPELVLPKPGASVEISIKASGYFFYYHMHKQSHVKSLWIGRNPYNGVTSY 60
QY      1  QVLQVQSGAEYKPKPGASVKYSCSKASGYTFEYYMYWVRQAFPGQGLELMGRIDPEDGSIDY 60
Db      61  NONFKDKASLTVDKSSSTAYMELHSLTSDSNAVYICARPTVD--FDYWGQGTTLTVSS 116
QY      61  VEKFKKVTITADTSSSTAYMELSSLLISDDTAVYICARGKFNRYAFYWGQGTTLTVSS 118

RESULT 14
ID      AC      P97771;      PRELIMINARY;      PRT;      241 AA.
DT      01-MAY-1997 (TREMBLREL. 03, CREATED)
DT      01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT      01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE      ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS      MUS. MUSCULUS (MOUSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; RODENTIA.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      CHUNG J.H., LEE S.D., YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.

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RA KIM I.J., CHOI I.H., CHUNG H.K.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U88067; G1850548;
DR PFAM: PF00047; 19.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; EBB2D29D CRC32;

Query Match 59.28; Score 507; DB 11; Length 241;

Best Local Similarity 56.3%; Pred. No. 3.78e-84;

Matches 67; Conservative 24; Mismatches 26; Indels 2; Gaps 2;

Db 1 QVQLQSGPELKKPGETVKISCKASGYFTDYGNNVYKQAPGKGLKWMGINTVYGEPTY 60

QY 1 QVQLVSGAEVKKPGASVKVSCRASGYFTFEYIMYWRQAPGGGLELMGRIDPDGSDY 60

Db 61 ADFKGRFAFSLETSASTAYLQINLNKNEATYFCARKDLLRY-FDYWGQGTITVYSS 118

QY 61 VERFKKKVLTADTSSSTAYMELSSLTSDTAVYTCARGKF-NYRFAYWGQGLTVYSS 118

RESULT 15

ID O55113 PRELIMINARY; PRT; 98 AA.

AC O55113;

DT 01-JUN-1998 (TREMELREL. 06, CREATED)

DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMELREL. 06, LAST ANNOTATION UPDATE)

DE A6 ANTI-[4-HYDROXY-3-NITROPHENYL(PHENOLATE FORM)] ACETYL NAB V-H

DE REGION (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57B2/6;

RX MEDLINE: 88198051.

RA SOBRANDRIO A., AZUMA T., HAMADA Y., SAKATO N., FUJIO H.;

RL J. BIOCHEM. 102:1337-1343(1987).

DR EMBL; D00233; D1019624; -

FT NON_TER 1

FT NON_TER 98

SQ SEQUENCE 98 AA; 10865 MW; 4C615AE9 CRC32;

Query Match

Best Local Similarity 71.1%; Pred. No. 1.72e-83;

Matches 69; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Db 1 QVQLQSGAEVLKPGASVKLSCKASGYFTSYWHVYKQRPGRGLEWIGRIDPNSGTTY 60

QY 1 QVQLVSGAEVKKPGASVKVSCRASGYFTFEYIMYWRQAPGGGLELMGRIDPDGSDY 60

Db 61 NEKFKSKATLTVDKPSSTAYMOLSSLSXSDSAVYCA 97

QY 61 VERFKKKVLTADTSSSTAYMELSSLTSDTAVYCA 97

Search completed: Thu Jan 14 17:14:12 1999

Job time : 25 secs.

(TM)

protein - protein database search, using Smith-Waterman algorithm

.....235:990..Million..cell..updates/sec

Title:
>US-08-477-989B-93

Perfect Score: 856
Sequence: 1 QVLVQSGAEVKKPGASVKV.....GRNYRFAYWGQGLTVYSS 118

Searched: 131922 seqs, 16180660 residues

Database: a-genesec32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	750	87.6	140 11	R59084	LO-CD2a VH and leader	4.61e-48
2	739	86.3	163 11	R59089	Protein encoded by re	3.46e-48
3	654	76.4	120 9	R24741	Humanised anti-CD18 A	1.96e-41
4	653	76.3	116 24	W24218	Reshaped human ADK12-	2.35e-41
5	653	76.3	135 6	R29017	pUC-RVH-1220d.	2.35e-41
6	653	76.3	135 6	R29016	pUC-RVH-1220b.	2.35e-41
7	648	75.7	120 25	W27551	Human Ab heavy chain	5.86e-41
8	642	75.0	139 7	R33953	gH1 variable domain.	1.75e-40
9	642	75.0	139 25	W29753	CDR-grafted humanised	1.75e-40
10	638	74.5	120 20	W05835	Humanised M291 antibo	3.63e-40
11	638	74.5	139 28	W36165	Humanised heavy chain	3.63e-40
12	638	74.5	279 20	W05836	Humanised M291 antibo	3.63e-40
13	632	73.8	382 25	W26651	Chimeric receptor hCT	1.08e-39
14	632	73.8	403 25	W26648	Chimeric receptor hCT	1.08e-39
15	632	73.8	473 25	W26646	Chimeric receptor hCT	1.08e-39
16	632	73.8	514 25	W26647	Chimeric receptor hCT	1.08e-39
17	632	73.8	651 25	W26649	Chimeric receptor hCT	1.08e-39
18	632	73.8	692 25	W26650	Chimeric receptor hCT	1.08e-39

KW	Monoclonal antibody; MAb; heavy chain; light chain; constant region; variable region; amplification; primer;
KW	polymerase chain reaction; PCR; chimera; Ig;
KW	immunoglobulin; humanised antibody; leucocyte; integrin.
OS	Chimeric: Homo sapiens.
OS	Chimeric: Mus sp.
PN	EP-578515-A.
PN	12-JAN-1994.
PF	24-MAY-1993; 401328.
PF	26-MAY-1992; US-888233.
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
PI	Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
DR	WPI; 94-010334/02.
DR	N-PSDB; Q54999.
PT	Humanised monoclonal antibodies prepn. - using comparative model
PT	building, by computer database searching
PT	Disclosure, page 18; 68pp; English.
PS	A humanised monoclonal antibody corresponding to the murine anti-CD18
CC	antibody 60.3 was prepared. The variable (V) region sequences from
CC	both the heavy (H) and light (L) chains were determined from cDNA
CC	(amplified by PCR), and spliced onto human constant (C) regions,
CC	resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC	expressed in tissue culture (A98.653 mouse myeloma cells, detected
CC	by ELISA), and examined in binding assays. The results from
CC	competition and inhibition assays showed that the chimeric Ab was
CC	as effective as the murine 60.3 MAb. The deduced murine VH and VL
CC	protein sequences were compared to the protein sequence data base,
CC	and two human Ig protein sequences were selected to be used as
CC	templates. A murine 60.3 Fv was modeled according to the deduced
CC	VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC	human template sequences selected from the protein data base, a
CC	humanised Fv was modeled. Construction of the humanised 60.3 was
CC	done by piecing 5 pairs of complementary oligonucleotides together
CC	(spanning the entire V region) to form the VH and VL. These were
CC	then attached onto vectors containing genes for appropriate C regions
CC	to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC	expressed in A98.653 cells and binding assays were done. FACS analyses
CC	indicated that the humanised Ab recognised cells expressing CD18.
CC	About a dozen of the humanised 60.3 Ab master wells were transferred
CC	and assayed for Ig.
CC	Sequence 120 AA;
SQ	
Query Match 76.4%; Score 654; DB 9; Length 120;	
Best Local Similarity 75.8%; Pred. No. 1.96e-41;	
Matches 91; Conservative 11; Mismatches 16; Indels 2; Gaps 2	
Db	1 qvqlvsgaevkpgasvkscasytftdyvmvvrqapggglwmgripdsdsethy 60
QY	1 QVQLVSGAEVKKPGASVKSCASGYTFTDYVMVVRQAPGGGLWLGRIPEDEGSIDY 60
Db	61 nqkfgrvtrtdtstymelsslrsedtavycarggrlqsfamdyvgqgtlvtvss 120
QY	61 VEFKKKVLTDTSSTAYMELSSLTSDTAVIYCARG-KF-NYRFAYWGQGLVTVSS 118
RESULT 4	
ID	W22418 standard; Protein; 116 AA.
AC	W22418;
DT	08-DEC-1997 (first entry)
KW	Reshaped human AUK12-20 VH.
KW	Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW	asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW	metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW	transplant rejection; graft versus host disease; nephritis;
KW	atopic dermatitis; psoriasis; myocardial ischaemia;
KW	acute leucocyte mediated lung injury; therapy; AUK12-20.
OS	Chimeric Homo sapiens;
OS	Chimeric synthetic.
FH	Key Location/Qualifiers
FT	region 1..30
FT	/label= FR1
FT	region 31..35
FT	/label= CDRI

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FT region 36..49
FT /label= FR2
FT region 50..66
FT /label= CDR2
FT region 67..98
FT /label= FR3
FT region 99..105
FT /label= CDR3
FT region 106..116
FT /label= FR4
FT WO9718838-A1.
PD 29-MAY-1997.
PE 21-NOV-1996: U18807.
PR 21-NOV-1995: US-561521.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
DR WPI; 97-297879/27.
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
PS Example 6; Page 44; 107pp; English.
CC This polypeptide comprises version 'b', of a reshaped human
CC antibody AUK12-20 VH region. A DNA fragment encoding the
CC polypeptide was subcloned into vector pUC19 for use as a template
CC for PCR amplification and production of version 'a' of a reshaped
CC human 21.6 VH region (see W22413) that can be used in the
CC construction of novel humanised anti-alpha-4 integrin antibodies.
CC Claimed humanised antibodies are useful in the treatment of
CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC bowel disease, rheumatoid arthritis, transplant rejection, graft
CC versus host disease, tumour metastasis, nephritis, atopic
CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC mediated lung injury.
SQ Sequence 116 AA;

Query Match 76.3%; Score 653; DB 24; Length 116;
Best Local Similarity 79.7%; Pred. No. 2.35e-41;
Matches 94; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

Db 1 qvqlvsgaevkpgasvkscasgysftsyihwvrgpaggglewgidpfnngtsy 60
QY 1 QVQLVSGAEVKPGASVKVSKRSGYTFTEYIMYWRQAPGGQLELMGRIDPEDGSIDY 60
Db 61 nqfkqkvtmtdstntaymelsslrsdttavycargg-n-rfaywgggtlvtvss 116
QY 61 VERFKKKVTLTADTSSTAYMELSSLTSDTAVYVCARGENRYFAWGGQTLTVSS 118

RESULT 5
ID R29017 standard; Protein; 135 AA.
AC R29017;
DT 30-MAR-1993 (first entry)
DE pUC-RVH-1220d.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19
FT /note= "Leader peptide"
FT region 20..49
FT /label= FR1
FT region 50..54
FT /label= CDR1
FT region 55..68
FT /label= FR2
FT region 69..85
FT /label= CDR2
FT region 86..117
FT /label= FR3
FT region 118..124
FT /label= CDR3
FT region 125..135
FT /label= FR4
PN WO9718838-A1.
PD 29-MAY-1997.
PE 21-NOV-1996: U18807.
PR 21-NOV-1995: US-561521.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
DR WPI; 97-297879/27.
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
PS Example 6; Page 44; 107pp; English.
CC This polypeptide comprises version 'b', of a reshaped human
CC antibody AUK12-20 VH region. A DNA fragment encoding the
CC polypeptide was subcloned into vector pUC19 for use as a template
CC for PCR amplification and production of version 'a' of a reshaped
CC human 21.6 VH region (see W22413) that can be used in the
CC construction of novel humanised anti-alpha-4 integrin antibodies.
CC Claimed humanised antibodies are useful in the treatment of
CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC bowel disease, rheumatoid arthritis, transplant rejection, graft
CC versus host disease, tumour metastasis, nephritis, atopic
CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC mediated lung injury.
SQ Sequence 116 AA;

Query Match 76.3%; Score 653; DB 24; Length 116;
Best Local Similarity 79.7%; Pred. No. 2.35e-41;
Matches 94; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

Db 1 qvqlvsgaevkpgasvkscasgysftsyihwvrgpaggglewgidpfnngtsy 60
QY 1 QVQLVSGAEVKPGASVKVSKRSGYTFTEYIMYWRQAPGGQLELMGRIDPEDGSIDY 60
Db 61 nqfkqkvtmtdstntaymelsslrsdttavycargg-n-rfaywgggtlvtvss 116
QY 61 VERFKKKVTLTADTSSTAYMELSSLTSDTAVYVCARGENRYFAWGGQTLTVSS 118

RESULT 5
ID R29017 standard; Protein; 135 AA.
AC R29017;
DT 30-MAR-1993 (first entry)
DE pUC-RVH-1220d.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19
FT /note= "Leader peptide"
FT region 20..49
FT /label= FR1
FT region 50..54
FT /label= CDR1
FT region 55..68
FT /label= FR2
FT region 69..85
FT /label= CDR2
FT region 86..117
FT /label= FR3
FT region 118..124
FT /label= CDR3
FT region 125..135
FT /label= FR4
PN WO9718838-A1.
PD 29-MAY-1997.
PE 21-NOV-1996: U18807.
PR 21-NOV-1995: US-561521.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
DR WPI; 97-297879/27.
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
PS Example 6; Page 44; 107pp; English.
CC This polypeptide comprises version 'b', of a reshaped human
CC antibody AUK12-20 VH region. A DNA fragment encoding the
CC polypeptide was subcloned into vector pUC19 for use as a template
CC for PCR amplification and production of version 'a' of a reshaped
CC human 21.6 VH region (see W22413) that can be used in the
CC construction of novel humanised anti-alpha-4 integrin antibodies.
CC Claimed humanised antibodies are useful in the treatment of
CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC bowel disease, rheumatoid arthritis, transplant rejection, graft
CC versus host disease, tumour metastasis, nephritis, atopic
CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC mediated lung injury.
SQ Sequence 116 AA;

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PN WO9219759-A.
PD 12-NOV-1992.
PE 24-APR-1992: J00544.
PR 25-APR-1991: JP-095476.
PR 19-FEB-1992: JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI; 92-398882/48.
DR N-PSDB; Q31391.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 159-60; 207pp; Japanese.
CC The sequences given in R29016-17 are portions of monoclonal antibodies
CC which were encoded by plasmids contained within the mouse hybridoma,
CC AUK12-20. The DNA encoding the complementarity determining regions
CC (CDR's) was isolated by polymerase chain reaction. These antibodies
CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells
CC were transformed with plasmids containing fragments of the antibody
CC gene which caused the production of the antibody from the hybridoma
CC cell line.
SQ Sequence 135 AA;

Query Match 76.3%; Score 653; DB 6; Length 135;
Best Local Similarity 79.7%; Pred. No. 2.35e-41;
Matches 94; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

Db 20 qvqlvsgaevkpgasvkscasgysftsyihwvrgpaggglewgidpfnngtsy 79
QY 1 QVQLVSGAEVKPGASVKVSKRSGYTFTEYIMYWRQAPGGQLELMGRIDPEDGSIDY 60
Db 80 nqfkqkvtmtdstntaymelsslrsdttavycargg-n-rfaywgggtlvtvss 135
QY 61 VERFKKKVTLTADTSSTAYMELSSLTSDTAVYVCARGENRYFAWGGQTLTVSS 118

RESULT 6
ID R29016 standard; Protein; 135 AA.
AC R29016;
DT 30-MAR-1993 (first entry)
DE pUC-RVH-1220b.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19
FT /note= "Leader peptide"
FT region 20..49
FT /label= FR1
FT region 50..54
FT /label= CDR1
FT region 55..68
FT /label= FR2
FT region 69..85
FT /label= CDR2
FT region 86..117
FT /label= FR3
FT region 118..124
FT /label= CDR3
FT region 125..135
FT /label= FR4
PN WO9219759-A.
PD 12-NOV-1992.
PE 24-APR-1992: J00544.
PR 25-APR-1991: JP-095476.
PR 19-FEB-1992: JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI; 92-398882/48.
DR N-PSDB; Q31391.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity

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FT	region	45..54	
FT	/label=	CDR1	
FT	region	69..85	
FT	/label=	CDR2	
FT	region	118..128	
FT	/label=	CDR3	
PN	EP-534742-A.		
PD	31-MAR-1993.		
PF	24-SEP-1992:	308680.	
PR	26-SEP-1991:	GB-020467.	
PA	(CLLT) CELLTech LTD.		
PI	Adair JR, Baker JS, Hamann PR, Hinman LM, Lyons AH;		
PI	Menendez AJ, Owens RJ;		
DR	WPI; 93-102837/13.		
DR	N-PSDB: Q38882-89.		
PT	Anti-human milk fat globule humanised antibodies - useful as		
PT	conjugate for in-vivo diagnosis and therapy of e.g. ovarian or		
PT	breast cancer		
PS	Disclosure: Page 27; 57pp; English.		
CC	This sequence represents the CDR-grafted heavy chain, gH1. This		
CC	protein is encoded by the DNA constructed using the oligonucleotides		
CC	given in Q38882-89. This heavy chain was used in conjunction with a		
CC	light chain (see also R33954) in the production of a humanised		
CC	antibody molecule (HAM). At least one of the complementarity		
CC	determining regions (CDR's) of the variable domain is derived from		
CC	the mouse monoclonal antibody (MAB) CTM01 and the remaining immuno-		
CC	globulin-derived parts of the HAM are derived from a human immuno-		
CC	globulin (or an analogue). The HAM was used for in vivo diagnosis and		
CC	therapy of carcinomas of ovary, breast, uterus and lung.		
SQ	Sequence 139 AA;		
Query Match 75.0%; Score 642; DB 7; Length 139;			
Best Local Similarity 73.3%; Pred. No. 1.75e-40;			
Matches 88; Conservative 14; Mismatches 16; Indels 2; Gaps 1;			
Db	20	qqlvqsgaevkpkssvskvscasgytfdyyinvmrqapqggilewmgwidpgsgntky 79	
QY	1	QVQLVQSGAEVKPKGASVSKVSCASYTFTYYMYVWRQAPGQGLELMGRIDPDGSDY 60	
Db	80	nekfgrvitvdtstntaymellsrsdtdafyfcarektyyyamdywgggtltvss 139	
QY	61	VEKFKKVVLTADTSSTAYMELSLTSDTAVYYCARGK--FNRYFAYWGQGLTVTSS 118	
RESULT	9		
ID	W29753 standard; Protein; 139 AA.		
AC	W29753;		
DE	14-JAN-1998 (first entry)		
DE	CDR-grafted humanised antibody heavy chain variable region gH1.		
DE	Humanised antibody; CDR-grafted antibody; chimeric antibody; CTM01;		
KW	complementarity determining region; human milk fat globule; HMFG;		
KW	monoclonal antibody; MAB; mouse; cancer; breast cancer;		
KW	ovary carcinoma; lung cancer; uterus cancer; diagnosis; therapy.		
OS	Chimeric Homo sapiens.		
OS	Chimeric Mus musculus.		
OS	Chimeric synthetic.		
Key	Location/Qualifiers		
FT	Region	45..54	
FT	/label=	CDR1	
FT	/note=	"complementarity determining region 1	
FT		from CTM01"	
FT	Region	69..85	
FT	/label=	CDR2	
FT	/note=	"complementarity determining region 2	
FT		from CTM01"	
FT	Region	118..128	
FT	/label=	CDR3	
FT	/note=	"complementarity determining region 3	
FT		from CTM01"	
FT	Misc-difference 2		
FT	/note=	"murine residue"	
FT	Misc-difference 37		
FT	/note=	"murine residue"	

FT	/note= "human framework residue 44 is substd. by
FT	equivalent murine_="framework residue"
FT	misc_difference 67
FT	/note= "human framework residue 67 is substd. by
FT	equivalent murine framework residue"
FT	misc_difference 68
FT	/note= "human framework residue 68 is substd. by
FT	equivalent murine framework residue"
FT	misc_difference 70
FT	/note= "human framework residue 70 is substd. by
FT	equivalent murine framework residue"
FT	misc_difference 72
FT	/note= "human framework residue 72 is substd. by
FT	equivalent murine framework residue"
FT	misc_difference 74
FT	/note= "human framework residue 74 is substd. by
FT	equivalent murine framework residue"
PN	W09G26964-Al.
PD	06-SEP-1996;
PD	29-FEB-1996; U02754.
PP	01-NAR-1995; US-397411.
PR	(IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
PA	(PROT-) PROTEIN DESIGN LABS INC.
PA	Gingrich R, Link BK, Tso JY, Weiner G;
PI	WPI: 96-412742/41.
DR	New bispecific antibody reactive with both T or NK cells and
PPT	malignant B cells - also their humanised forms and hybridomas
PPT	producing them, useful for treating or preventing leukaemia,
PPT	lymphoma and myeloma
PS	Claim 18; Fig 5b; 85pp; English.
PS	The variable region (W05825) of the humanised M291 antibody heavy
CC	-chain (W03826) consists of human H2-1/17 heavy chain variable
CC	region framework and complementarity determining regions from the
CC	murine M291 antibody specific for CD3 antigen. It can be
CC	coexpressed with humanised M291 light chain (see also W05830) in
CC	mammalian host cells. Humanised antibody fragments can be
CC	incorporated into novel bispecific antibodies reactive with both
CC	effector cell antigens and malignant B-cells (see also W05822-23).
CC	W05828-29).
SQ	Sequence 120 AA:

Query Match	74.5%	Score 638;	DB 20;	Length 120;
Best Local Similarity	76.7%;	Pred. No. 3.63e-40;		
Matches	92;	Conservative 8;	Mismatches 18;	Indels 2;
				Gaps 2;

Db	1	qvolvqsgaevkpkpaasvkvsckasgyffislytmhvwgagpgglwmgynprsgythy	60
QY	1	QVOLVQSGAEVKKPKGASVKVSKASGYTFTEYIMVYVWRAQPGQGLMGRIDPEDGSIDY	60
Db	61	ngklkdkaatlckdaasatymelslrtsedavvycaasaydydgfaywgqgtlvtvss	120
QY	61	VSKFKKKVLTADTSSSYAYMELSLTSDTAVYCAKGKF-NYR-FAYWGQGTLTVTSS	118

RESULT 11
ID W36165 standard; Protein: 139 AA.

DT 22-MAY-1998 (first entry)
DE Humanised heavy chain variable region of mouse M291 antibody.
DE Heavy chain; variable region; low mitogenic response; human T-cell;
KW immunosuppressant; diagnosis; immune system disease; antibody M291;
KW humanised; mouse; murine.

[illegible]

FI WO9744362-A1.
PN 27-NOV-1997.
PD

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PF 19-MAY-1997; U08576.
PR 31-MAY-1996; US-656586.
PR 20-MAY-1996; US-650410.
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
PA (PROT-) PROTEIN DESIGN LABS INC.
PI Anasetti C, Cole MS, Tso JY;
DR WPI: 98-018436/02.
DR N-PSDB: V01095.
PT Mutated immunoglobulin G 2 constant region that does not induce T
PT cell proliferation - and anti-CD3 antibodies containing this region
PT for use as immunosuppressant with reduced side effects
PS Claim 11: Fig 1D; 63pp; English.
CC The present sequence was used in the development of a novel mutated
CC immunoglobulin G (IgG) 2 constant region (CR); having a non-natural
CC segment of amino acids between 234 and 237 (EU numbering system),
CC so that an antibody (Ab) containing the variable region of an
CC anti-CD3 Ab linked to the CR induces lower mitogenic response in
CC human T-cells than does a similar Ab containing the natural IgG2
CC constant region.
CC The Ab are useful as immunosuppressants, e.g. in autoimmune
CC disease (including rheumatoid arthritis, multiple sclerosis, type I
CC diabetes, systemic lupus erythematosus and inflammatory bowel
CC disease), transplant rejection, graft versus host disease,
CC inflammation allergy or sepsis, particularly acute episodes of
CC autoimmune diseases. The Ab can also be used for diagnosis of
CC immune system disease and for determining T cell numbers in
CC patients with acquired immune deficiency syndrome (AIDS).
CC The Ab have fewer side effects than known anti-CD3 Ab, as they do
CC not, in most patients, induce mitogenesis through specific binding
CC to FC gamma receptors, nor release of cytokines. Compared with
CC Fab'2 fragments, the Ab have a longer half-life.
CC Sequence 139 AA;
SQ
Query Match 74.5%; Score 638; DB 28; Length 139;
Best Local Similarity 76.7%; Pred. No. 3.63e-40;
Matches 92; Conservative 8; Mismatches 18; Indels 2; Gaps 2;

Db 20 qvqlvsgaevkpgasvkscasgytfisyltmhwrqagpgqlwngylnprsgythy 79
QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFEYIMYVWVRQPGQLEMLGRIDPDGSIDY 60

Db 80 nqklkdktltdaksastaymellsrsdtaavyrcarsaydydgfwgggtlvtvss 139
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAIVYVYCARCKF-NYR-FAYWGGQGLTVTVSS 118

RESULT 12
ID W05826;
AC W05826;
DE 27-JAN-1997 (first entry)
KW CD3 antigen; humanised antibody; bispecific antibody;
KW B-cell lymphoma; myeloma; leukaemia; hybridoma;
KW monoclonal antibody.
OS Chimeric Homo sapiens;
OS Chimeric Mus sp.
FH Key Location/Qualifiers
FT domain 1..120
FT /label= Variable_domain
FT region 31..35
FT /label= CDR1
FT region 50..66
FT /label= CDR2
FT region 79..109
FT /label= CDR3
FT misc_difference 30
FT /note= "human framework residue 30 is substd. by
FT equivalent murine framework residue"
FT misc_difference 44
FT /note= "human framework residue 44 is substd. by
FT equivalent murine framework residue"
FT misc_difference 67
FT /note= "human framework residue 67 is substd. by

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FT misc_difference 68
FT /note= "human framework residue 68 is substd. by
FT equivalent murine framework residue"
FT misc_difference 70
FT /note= "human framework residue 70 is substd. by
FT equivalent murine framework residue"
FT misc_difference 72
FT /note= "human framework residue 72 is substd. by
FT equivalent murine framework residue"
FT misc_difference 74
FT /note= "human framework residue 74 is substd. by
FT equivalent murine framework residue"
FT domain 121..218
FT /label= CH1_domain
FT domain 219..238
FT /label= Hinge_domain
FT domain 239..279
FT /label= Fc_leucine_zipper
FN W09626964-A1.
PN 06-SEP-1996.
PD 29-FEB-1996; U02754.
PF 01-MAR-1995; US-397411.
PR (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
PA (PROT-) PROTEIN DESIGN LABS INC.
PI Gingrich R, Link BK, Tso JY, Weiner G;
DR WPI: 96-412742/41.
PT New bispecific antibody reactive with both T or NK cells and
PT malignant B cells - also their humanised forms and hybridomas
PT producing them, useful for treating or preventing leukaemia,
PT lymphoma and myeloma
PT Claim 28; Fig 5d; 85pp; English.
PS The humanised M291 antibody heavy chain (W05826) includes a
CC variable region (see also W05825) consisting of human HF2-1/17
CC heavy chain variable region framework and complementarity
CC determining regions from the murine M291 antibody specific for CD3
CC antigen. It can be coexpressed with humanised M291 light chain (see
CC also W05830) in mammalian host cells. Bispecific antibodies can
CC be constructed that include a first binding fragment comprising
CC humanised M291 heavy and light chain variable regions, and a second
CC binding fragment comprising humanised 1D10 heavy and light chain
CC variable regions (see also W05828-29). Such antibodies are reactive
CC with both T or NK cells and malignant B cells, and have therapeutic
CC and diagnostic applns.
SQ Sequence 279 AA;

Query Match 74.5%; Score 638; DB 20; Length 279;
Best Local Similarity 76.7%; Pred. No. 3.63e-40;
Matches 92; Conservative 8; Mismatches 18; Indels 2; Gaps 2;

Db 1 qvqlvsgaevkpgasvkscasgytfisyltmhwrqagpgqlwngylnprsgythy 60
QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFEYIMYVWVRQPGQLEMLGRIDPDGSIDY 60

Db 61 nqklkdktltdaksastaymellsrsdtaavyrcarsaydydgfwgggtlvtvss 120
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAIVYVYCARCKF-NYR-FAYWGGQGLTVTVSS 118

RESULT 13
ID W26651;
AC W26651;
DE 12-FEB-1998 (first entry)
KW Chimeric receptor hCTM01/h/zeta.
KW Cell activation; chimeric receptor; DNA delivery; CTM01; scFv;
KW IgG1; T cell receptor zeta chain; cell proliferation; cytokine;
KW inflammation; effector; cell differentiation; antibody secretion;
KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
KW graft versus host disease; human; therapy.
OS Chimeric - Homo sapiens.

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WO9723613-A2.
 PD 03-JUL-1997.
 PF 23-DEC-1996; G03209.
 PR 21-DEC-1995; GB-026131.
 PA (CLLT) CELTECH THERAPEUTICS LTD.
 PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;
 DR WPI: 97-351052/32.
 DR N-PSDB; T90514.
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 PS Disclosure; Fig 9; 90pp; English.
 CC This protein comprises a chimeric receptor consisting of an scFv
 CC engineered from anti-CD3 human antibody CTM01 linked to an
 CC extracellular spacer comprising the human IgG1 hinge, part of the
 CC extracellular region of human CD28 and 4 amino acid residues, linked
 CC to the transmembrane and intracellular regions of the human T cell
 CC receptor zeta chain. It can be expressed in host (e.g. Jurkat)
 CC cells using a chimeric receptor gene (see T90514) constructed from
 CC DNA cassettes encoding each component of the receptor. In a
 CC cell activation process an effector cell is transformed with DNA
 CC encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/idiopathic disease (claimed).
 CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease or diabetes (claimed).
 SQ Sequence 382 AA;
 Query Match 73.8%; Score 632; DB 25; Length 382;
 Best Local Similarity 72.5%; Pred. No. 1.08e-39;
 Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;
 Db 160 qqlvqsgaevkpgssvkscasgyftdyinwmrqapggglwlgwldpgsgntky 219
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYIMYWRQAPGQGLMGRIDPDGSDY 60
 Db 220 nekfgkgratltvdstntaymelssrdsdtafcarektttyyamydgwgggtlvtvss 279
 QY 61 VERFKKRVTLTADTSSSTAYMELSSLTSDTAVYICARGK--FNRYFAYWGQGLTVTVSS 118
 RESULT 14
 ID W26648 standard; Protein; 403 AA.
 AC W26648;
 DE 12-FEB-1998 (first entry)
 KW Chimeric receptor hCTM01/CD8/CD28
 KW Cell activation; chimeric receptor; DNA delivery; CTM01; scFv; CD8;
 KW CD26; cell proliferation; cytokine; inflammation; effector;
 KW cell differentiation; antibody secretion; phagocytosis;
 KW tumour infiltration; adhesion; infection; cancer; allergy;
 KW rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.
 OS Chimeric - Homo sapiens.
 PN WO9723613-A2.
 PD 03-JUL-1997.
 PF 23-DEC-1996; G03209.
 PR 21-DEC-1995; GB-026131.
 PA (CLLT) CELTECH THERAPEUTICS LTD.
 PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;

DR WPI: 97-351052/32.
 DR N-PSDB; T90511.
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 PS Disclosure; Fig 6; 90pp; English.
 CC This protein comprises a chimeric receptor consisting of an scFv
 CC engineered from anti-CD3 human antibody CTM01 linked to an
 CC extracellular spacer from part of human CD8 hinge, linked to the
 CC extracellular and intracellular components of human CD28. It can
 CC be expressed in host cells using a chimeric receptor gene (see
 CC T90511) constructed from DNA cassettes of each component. In a
 CC claimed cell activation process an effector cell is transformed with
 CC DNA encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/idiopathic disease (claimed).
 CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease or diabetes (claimed).
 SQ Sequence 403 AA;
 Query Match 73.8%; Score 632; DB 25; Length 403;
 Best Local Similarity 72.5%; Pred. No. 1.08e-39;
 Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;
 Db 160 qqlvqsgaevkpgssvkscasgyftdyinwmrqapggglwlgwldpgsgntky 219
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYIMYWRQAPGQGLMGRIDPDGSDY 60
 Db 220 nekfgkgratltvdstntaymelssrdsdtafcarektttyyamydgwgggtlvtvss 279
 QY 61 VERFKKRVTLTADTSSSTAYMELSSLTSDTAVYICARGK--FNRYFAYWGQGLTVTVSS 118
 RESULT 15
 ID W26646 standard; Protein; 473 AA.
 AC W26646;
 DE 12-FEB-1998 (first entry)
 KW Chimeric receptor hCTM01/CD8/zeta.
 KW Cell activation; chimeric receptor; DNA delivery; CTM01; scFv; CD8;
 KW T cell receptor zeta chain; cell proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.
 OS Chimeric - Homo sapiens.
 PN WO9723613-A2.
 PD 03-JUL-1997.
 PF 23-DEC-1996; G03209.
 PR 21-DEC-1995; GB-026131.
 PA (CLLT) CELTECH THERAPEUTICS LTD.
 PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;
 DR WPI: 97-351052/32.
 DR N-PSDB; T90509.
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 PS Disclosure; Fig 4; 90pp; English.
 CC This protein comprises a chimeric receptor consisting of an scFv
 CC engineered from anti-CD3 human antibody CTM01 linked to an

CC extracellular spacer in the form of part of human CD8 hinge, linked
 CC to the extracellular, transmembrane and intracellular components of
 CC the human T cell receptor zeta chain. It can be expressed in host
 CC cells (e.g. Jurkat) using a chimeric receptor gene (see T90509)
 CC constructed from DNA cassettes of each component. In a claimed
 CC cell activation process an effector cell is transformed with DNA
 CC encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/diopathic disease (claimed).
 CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease or diabetes (claimed).
 SQ Sequence 473 AA;

Query Match 73.8%; Score 632; DB 25; Length 473;
 Best Local Similarity 72.5%; Pred. No. 1.08e-39;
 Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;
 Db 160 qqlvqsgaevkpgsvkvscksgyftdyvnmrqapqgglewlgwidpssgntky 219
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYMYWVRQAPGQGLELMGRIDPDGSDY 60
 Db 220 nekfkgratlvtstntaymelslrsedtafyfcarektyvyamdywgqgtlvtvss 279
 QY 61 VEKFKKVTTLTADISSAYMELSSLSDDTAVYICARGK--FNRYFAYWGQGLVTVSS 118

Search completed: Thu Jan 14 17:15:38 1999
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